

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 06:07:38 ; Search time 521.76 Seconds  
(without alignments)  
727.227 Million cell updates/sec

Title: US-09-846-456-4  
Perfect score: 221  
Sequence: 1 gtaattgcgagcgagagtga.....aacacaaaagtgaacacag 221

Scoring table: OLIGO.NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_032802.\*  
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.\*  
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	221	100.0	7260	22 AAD21326	Human ATP binding
2	221	100.0	7260	22 AAI70315	Human ATP binding
3	219	99.1	763	22 AAH04729	Human CDNA clone (
4	219	99.1	1750	22 AAH17451	Human CDNA sequenc
5	217	98.2	736	22 AAH07432	Human CDNA clone (
6	217	98.2	1536	22 AAH18606	Human CDNA sequenc
7	205	92.8	7086	22 ABA09200	Human ABCA1 homolo
8	205	92.8	7086	22 AAK52667	Human polynucleoti
9	205	92.8	7281	22 AAK51683	Human polynucleoti

10	205	92.8	9854	22 AAS06121	Human ABC1 DNA seq
11	201	183999	22	AAF92831	Human ABC1 genomic
12	197	89.1	227	21 AAC09615	Human secreted pro
13	197	89.1	10442	22 AAF24680	Nucleotide sequenc
14	197	89.1	10442	22 AAF24702	Nucleotide sequenc
15	188	85.1	10474	22 AAF24685	Nucleotide sequenc
16	188	85.1	10474	22 AAF24686	Nucleotide sequenc
17	188	85.1	10474	22 AAF24707	Nucleotide sequenc
18	188	85.1	10474	22 AAF24708	Nucleotide sequenc
19	92	41.6	446	22 AAS04035	Partial human ABC1
20	92	41.6	9741	22 AAS06120	Human ABC1 DNA seq
21	91	41.2	1643	22 AAF24681	Nucleotide sequenc
22	91	41.2	1643	22 AAF24703	Nucleotide sequenc
c 23	19	8.6	310	21 AAC00305	Human secreted pro
c 24	19	8.6	447	20 AAV90187	EST clone DH318.
c 25	19	8.6	710	11 AAQ06308	Sequence of DNA fr
c 26	19	8.6	735	15 AAQ73229	Soluble human inte
c 27	19	8.6	2184	11 AAQ06301	Sequence encoding
c 28	18	8.1	367	21 AAC13639	Human secreted pro
c 29	18	8.1	710	22 AAF58344	Human GTP-binding
c 30	18	8.1	758	21 AAF15226	Trichoderma reesei
c 31	18	8.1	1166	23 AAS68374	DNA encoding novel
c 32	18	8.1	1287	23 AAS72684	DNA encoding novel
c 33	18	8.1	1656	15 AAQ66990	5' flanking region
c 34	18	8.1	1725	15 AAQ66988	Human nervous syst
c 35	18	8.1	2484	22 ABA20286	Human nervous syst
c 36	18	8.1	2484	22 ABA20287	Human nervous syst
c 37	18	8.1	2779	21 AAZ88925	Netrin-2 coding se
c 38	18	8.1	2783	16 AAQ92367	Chick p75 cDNA. G
c 39	18	8.1	9248	20 AAZ32011	Human METH1 relate
c 40	18	8.1	9248	22 AAC90068	AB001735 cDNA clon
c 41	18	8.1	17294	24 ABL32987	Human immune syste
c 42	18	8.1	21436	22 AAK70011	Human immune/haema
c 43	18	8.1	21436	22 AAK73799	Human immune/haema
c 44	17	7.7	17	22 AAF92943	Wild type sequence
c 45	17	7.7	125	22 AAK90657	Human digestive sy

## ALIGNMENTS

RESULT	1
AAD21326	
ID	AAD21326 standard; DNA; 7260 BP.
XX	
AC	AAD21326;
XX	
DT	28-JAN-2002 (first entry)
XX	
DE	Human ATP binding cassette transporter 1 (ABC1) gene.
XX	
KW	Human; ATP binding cassette transporter 1; ABC1; coronary heart disease; dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
CDS	321..7106
FT	/tag=
FT	/product= "Human ABC1 protein"
XX	
PN	EP1136552-A1.
XX	
PD	26-SEP-2001.
XX	
PF	20-MAR-2000; 2000EP-0105820.
XX	
PR	20-MAR-2000; 2000EP-0105820.
XX	
PA	(FARB ) BAYER AG.
XX	





CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX  
 SQ Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;

Query Match 99.1%; Score 219; DB 22; Length 1750;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-102;  
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 aattgcgagcagagtgagtgaggcgccgagccgagcagcagccgagcccttctctcc 62  
 Db 1 aattgcgagcagagtgagtgaggcgccgagccgagcagccgagcccttctctcc 60  
 QY 63 gggtcgtcgcagggcagggcgccgagcctccgcgacacacagagcgggtctcaggcgcc 122  
 Db 61 gggtcgtcgcagggcagggcgccgagcctccgcgacacacagagcgggtctcaggcgcc 120  
 QY 123 ttgtcctctgtttttcccccgttctgtttctccttctcctcgaaggcttgcgaagg 182  
 Db 121 ttgtcctctgtttttcccccgttctgtttctccttctcctcgaaggcttgcgaagg 180  
 QY 183 ggtaggagaagagcagcagcaacacacaaaagtggaaaacag 221  
 Db 181 ggtaggagaagagcagcagcaacacacaaaagtggaaaacag 219

RESULT 5  
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 ID AAH07432 standard; cDNA; 736 BP.  
 XX  
 AC AAH07432;  
 XX  
 DT 26-JUN-2001 (first entry)  
 XX  
 DE Human cDNA clone (5'-primer) SEQ ID NO:4267.  
 XX  
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1074617-A2.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000EP-0116126.  
 XX  
 PR 29-JUL-1999; 99JP-0248036.  
 XX  
 PR 27-AUG-1999; 99JP-0300253.  
 XX  
 PR 11-JAN-2000; 2000JP-0118776.  
 XX  
 PR 02-MAY-2000; 2000JP-0183767.  
 XX  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX  
 XX (HELI-) HELIX RES INST.

PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 DR WPI; 2001-318749/34.  
 XX  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX

SQ Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;

Query Match 98.2%; Score 217; DB 22; Length 736;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-101;  
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 ttgcgagcagagtgagtgaggcgccgagccgagcagccgagcccttctctccgg 64  
 Db 5 ttgcgagcagagtgagtgaggcgccgagccgagcagccgagcccttctctccgg 64  
 QY 65 gctcggcagggcagggcgccgagcctccgcgacacacagagcgggtctcaggcgctt 124  
 Db 65 gctcggcagggcagggcgccgagcctccgcgacacacagagcgggtctcaggcgctt 124  
 QY 125 tgcctctgtttttcccccgttctgtttctccttctcctcgaaggcttgcgaagg 184  
 Db 125 tgcctctgtttttcccccgttctgtttctccttctcctcgaaggcttgcgaagg 184  
 QY 185 taggagaaagagcagcagcaacacaaaagtggaaaacag 221  
 Db 185 taggagaaagagcagcagcaacacaaaagtggaaaacag 221

RESULT 6  
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 ID AAH18606 standard; cDNA; 1556 BP.  
 XX  
 AC AAH18606;  
 XX  
 DT 26-JUN-2001 (first entry)  
 XX  
 DE Human cDNA sequence SEQ ID NO:18808.  
 XX  
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1074617-A2.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000EP-0116126.  
 XX  
 PR 29-JUL-1999; 99JP-0248036.  
 XX  
 PR 27-AUG-1999; 99JP-0300253.  
 XX  
 PR 11-JAN-2000; 2000JP-0118776.  
 XX  
 PR 02-MAY-2000; 2000JP-0183767.  
 XX  
 PR 09-JUN-2000; 2000JP-0241899.



```

CC novel human polypeptide of the invention.
XX Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
SQ

Query Match          92.8%; Score 205; DB 22; Length 7086;
Best Local Similarity 100.0%; Pred. No. 4.5e-95;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 gtgagtggggccgggacccgcagagccgagccgaccttctccgggctcgcgcaggg 76
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Db 7 gtgagtggggccgggacccgcagagccgagccgaccttctccgggctcgcgcaggg 66
   |||||||

QY 77 caggcggggagctccgcgcacacagagccggttctcaggcgcttgcctctgttt 136
   |||||||
Db 67 caggcggggagctccgcgcacacagagccggttctcaggcgcttgcctctgttt 126
   |||||||

QY 137 ttccccgggttctgttttctcccttctccggaaggttgcaggaggtaggagaaag 196
   |||||||
Db 127 ttccccgggttctgttttctcccttctccggaaggttgcaggaggtaggagaaag 186
   |||||||

QY 197 acgcaaacacaaagtggaaaacag 221
   |||||||
Db 187 acgcaaacacaaagtggaaaacag 211

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AAK52667
ID AAK52667 standard; cdna; 7086 BP.
XX
AC AAK52667;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2196.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
XX
PR 27-APR-2000; 2000US-0560875.
XX
PR 20-JUN-2000; 2000US-0598075.
XX
PR 19-JUL-2000; 2000US-0620325.
XX
PR 01-SEP-2000; 2000US-0654936.
XX
PR 15-SEP-2000; 2000US-0663561.
XX
PR 20-OCT-2000; 2000US-0693325.
XX
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR P-PSDB; AAM79534.
XX
Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 1; Page 4558-4560; 6221pp; English.
XX
The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC

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CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 4.5e-95;
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Db 7 gtgagtggggccgggacccgcagagccgagccgaccttctccgggctcgcgcaggg 66
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QY 77 caggcggggagctccgcgcacacagagccggttctcaggcgcttgcctctgttt 136
   |||||||
Db 67 caggcggggagctccgcgcacacagagccggttctcaggcgcttgcctctgttt 126
   |||||||

QY 137 ttccccgggttctgttttctcccttctccggaaggttgcaggaggtaggagaaag 196
   |||||||
Db 127 ttccccgggttctgttttctcccttctccggaaggttgcaggaggtaggagaaag 186
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QY 197 acgcaaacacaaagtggaaaacag 221
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Db 187 acgcaaacacaaagtggaaaacag 211

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ID AAK51683 standard; cdna; 7281 BP.
XX
AC AAK51683;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 228.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
XX
PR 27-APR-2000; 2000US-0560875.
XX
PR 20-JUN-2000; 2000US-0598075.
XX
PR 19-JUL-2000; 2000US-0620325.
XX
PR 01-SEP-2000; 2000US-0654936.
XX
PR 15-SEP-2000; 2000US-0663561.
XX
PR 20-OCT-2000; 2000US-0693325.
XX
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI

```





OS Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 291..7076  
 XX /\*tag= a  
 XX /product= "ABCl polypeptide"  
 XX WO200078972-A2.  
 XX 28-DEC-2000.  
 XX 16-JUN-2000; 2000WO-US16765.  
 XX 18-JUN-1999; 99US-0140264.  
 XX 14-SEP-1999; 99US-0153872.  
 XX 19-NOV-1999; 99US-0166573.  
 XX (CVTH-) CV THERAPEUTICS INC.  
 XX Lawn RM, Wade D, Garvin M;  
 XX WPI; 2001-137812/14.  
 XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 XX useful for the development of agents for the treatment of heart disease  
 XX and other disorders associated with hypercholesterolemia and  
 XX atherosclerosis -  
 XX Disclosure; Page 122-128; 215pp; English.  
 XX The present sequence encodes a human adenosine triphosphate (ATP)  
 XX binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
 XX membranes and utilises ATP hydrolysis to transport a wide variety of  
 XX substrates across the plasma membrane. ABC1 is a pivotal protein in  
 XX the apolipoprotein-mediated mobilisation of intracellular cholesterol  
 XX stores. ABC1 is defective in Tangier disease, a genetic disorder  
 XX characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
 XX localised to chromosome 9q22-9q31. The ABC1 genes and proteins are  
 XX useful for developing pharmaceutical agents for the treatment of heart  
 XX disease and other disorders associated with hypercholesterolemia and  
 XX atherosclerosis. The genes are useful for developing screening assays to  
 XX screen for compounds that regulate the expression of genes associated  
 XX with cholesterol transport. The genes and proteins are also useful for  
 XX are also useful as diagnostic indicators of cardiovascular disease and  
 XX other disorders associated with hypercholesterolemia.  
 XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;  
 XX  
 XX Query Match 89.1%; Score 197; DB 22; Length 10442;  
 XX Best Local Similarity 100.0%; Prod. No. 5.5e-91;  
 XX Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 QY 85 ggagctccgcgcaccacagagccggttctcagggcgcttctctctttttcccg 144  
 Db 61 ggagctccgcgcaccacagagccggttctcagggcgcttctctctttttcccg 120  
 QY 145 gtctgttttctcccttctccggaaggcttctcaggggttaggaaagacgcaaac 204  
 Db 121 gtctgttttctcccttctccggaaggcttctcaggggttaggaaagacgcaaac 180  
 QY 205 acaaaagtggaaacag 221  
 Db 181 acaaaagtggaaacag 197  
 RESULT 14  
 AAF24702  
 ID AAF24702 standard; DNA; 10442 BP.

XX AAF24702;  
 XX 20-APR-2001 (first entry)  
 XX Nucleotide sequence of a human ABC1 polypeptide.  
 XX Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 XX apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 XX chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 XX atherosclerosis; cholesterol transport; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 291..7076  
 XX /\*tag= a  
 XX /product= "ABCl polypeptide"  
 XX WO200078971-A2.  
 XX 28-DEC-2000.  
 XX 16-JUN-2000; 2000WO-US16591.  
 XX 18-JUN-1999; 99US-0140264.  
 XX 14-SEP-1999; 99US-0153872.  
 XX 19-NOV-1999; 99US-0166573.  
 XX (CVTH-) CV THERAPEUTICS INC.  
 XX (UNIW ) UNIV WASHINGTON.  
 XX Lawn RM, Wade D, Oram JF, Garvin M;  
 XX WPI; 2001-137811/14.  
 XX P-PSDB; AAB31365.  
 XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
 XX polynucleotides and polypeptides, useful for treatment of heart disease  
 XX and other disorders associated with hypercholesterolemia and  
 XX atherosclerosis -  
 XX Claim 3; Page 117-123; 211pp; English.  
 XX The present sequence encodes a human adenosine triphosphate (ATP)  
 XX binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
 XX membranes and utilises ATP hydrolysis to transport a wide variety of  
 XX substrates across the plasma membrane. ABC1 is a pivotal protein in  
 XX the apolipoprotein-mediated mobilisation of intracellular cholesterol  
 XX stores. ABC1 is defective in Tangier disease, a genetic disorder  
 XX characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
 XX localised to chromosome 9q22-9q31. The ABC1 genes and proteins are  
 XX useful for developing pharmaceutical agents for the treatment of heart  
 XX disease and other disorders associated with hypercholesterolemia and  
 XX atherosclerosis. The genes are useful for developing screening assays to  
 XX screen for compounds that regulate the expression of genes associated  
 XX with cholesterol transport. The genes and proteins are also useful for  
 XX are also useful as diagnostic indicators of cardiovascular disease and  
 XX other disorders associated with hypercholesterolemia.  
 XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;  
 XX  
 XX Query Match 89.1%; Score 197; DB 22; Length 10442;  
 XX Best Local Similarity 100.0%; Prod. No. 5.5e-91;  
 XX Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 25 ggcgggaccgcagagccgagccgaccttctctccgggctgcgagcaggcg 84  
 Db 1 ggcgggaccgcagagccgagccgaccttctctccgggctgcgagcaggcg 60  
 QY 85 ggagctccgcgcaccacagagccggttctcagggcgcttctctctttttcccg 144  
 Db 61 ggagctccgcgcaccacagagccggttctcagggcgcttctctctttttcccg 120  
 QY 145 gtctgttttctcccttctccggaaggcttctcaggggttaggaaagacgcaaac 204  
 Db 121 gtctgttttctcccttctccggaaggcttctcaggggttaggaaagacgcaaac 180  
 QY 205 acaaaagtggaaacag 221  
 Db 181 acaaaagtggaaacag 197  
 RESULT 14  
 AAF24702  
 ID AAF24702 standard; DNA; 10442 BP.



CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
CC Tangier disease, a genetic disorder characterised by abnormal  
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
CC pharmaceutical agents for the treatment of heart disease and other  
CC disorders associated with hypercholesterolemia and atherosclerosis. The  
CC genes are useful for developing screening assays to screen for compounds  
CC that regulate the expression of genes associated with cholesterol  
CC transport. The genes and proteins are also useful for are also useful  
CC as diagnostic indicators of cardiovascular disease and other disorders  
CC associated with hypercholesterolemia.  
XX  
SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 85.1%; Score 188; DB 22; Length 10474;  
Best Local Similarity 100.0%; Pred. No. 2.2e-86;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 ccgacagccgagccgacccctctctccgggctcgccgagcgagcgagcgagctccg 93  
|||||  
Db 42 ccgacagccgagccgacccctctctccgggctcgccgagcgagcgagcgagctccg 101  
QY 94 cgcacacacagagccggttcagggcgtttgctcctgtttttcccggttctgttt 153  
|||||  
Db 102 cgcacacacagagccggttcagggcgtttgctcctgtttttcccggttctgttt 161  
QY 154 tctcccttctcggagagcgttgtaggggtaggagaaagagcagcaacacaaagt 213  
|||||  
Db 162 tctcccttctcggagagcgttgtaggggtaggagaaagagcagcaacacaaagt 221  
QY 214 gaaaacag 221  
|||||  
Db 222 gaaaacag 229

RESULT 17  
ID AAF24707 standard; DNA; 10474 BP.  
XX  
AC AAF24707;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
KW atherosclerosis; cholesterol transport; ss.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
XX CDS 323..7108  
XX /\*tag= a  
XX /product= "defective ABC1 polypeptide"  
XX  
XX WO200078971-A2.  
XX  
XX 28-DEC-2000.  
XX  
XX 16-JUN-2000; 2000WO-US16591.  
XX  
XX 18-JUN-1999; 99US-0140264.  
XX 14-SEP-1999; 99US-0153872.  
XX 19-NOV-1999; 99US-0166573.  
XX  
XX (CVTH-) CV THERAPEUTICS INC.  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Lawn RM, Wade D, Oram JF, Garvin M;

XX WPI: 2001-137811/14.  
DR P-PSDB; AAB31366.  
XX  
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
PT polynucleotides and polypeptides, useful for treatment of heart disease  
PT and other disorders associated with hypercholesterolemia and  
PT atherosclerosis -  
XX  
PS Claim 27; Page 144-150; 211pp; English.  
XX  
CC The present sequence encodes a human adenosine triphosphate (ATP)  
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
CC ATP hydrolysis to transport a wide variety of substrates across the  
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
CC Tangier disease, a genetic disorder characterised by abnormal  
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
CC pharmaceutical agents for the treatment of heart disease and other  
CC disorders associated with hypercholesterolemia and atherosclerosis. The  
CC genes are useful for developing screening assays to screen for compounds  
CC that regulate the expression of genes associated with cholesterol  
CC transport. The genes and proteins are also useful for are also useful  
CC as diagnostic indicators of cardiovascular disease and other disorders  
CC associated with hypercholesterolemia.  
XX  
SQ Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match 85.1%; Score 188; DB 22; Length 10474;  
Best Local Similarity 100.0%; Pred. No. 2.2e-86;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 34 ccgacagccgagccgacccctctctccgggctcgccgagcgagcgagcgagctccg 93  
|||||  
Db 42 ccgacagccgagccgacccctctctccgggctcgccgagcgagcgagcgagctccg 101  
QY 94 cgcacacacagagccggttcagggcgtttgctcctgtttttcccggttctgttt 153  
|||||  
Db 102 cgcacacacagagccggttcagggcgtttgctcctgtttttcccggttctgttt 161  
QY 154 tctcccttctcggagagcgttgtaggggtaggagaaagagcagcaacacaaagt 213  
|||||  
Db 162 tctcccttctcggagagcgttgtaggggtaggagaaagagcagcaacacaaagt 221  
QY 214 gaaaacag 221  
|||||  
Db 222 gaaaacag 229

RESULT 18  
ID AAF24708 standard; DNA; 10474 BP.  
XX  
AC AAF24708;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
KW atherosclerosis; cholesterol transport; ss.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 323..7108  
XX /\*tag= a  
XX /product= "defective ABC1 polypeptide"  
XX

XX PN WO200078971-A2.  
 XX PD 28-DEC-2000.  
 XX PF 16-JUN-2000; 2000WO-US16591.  
 XX PR 18-JUN-1999; 99US-0140264.  
 XX PR 14-SEP-1999; 99US-0153872.  
 XX PR 19-NOV-1999; 99US-0166573.  
 XX PA (CVTH-) CV THERAPEUTICS INC.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PI Lawn RM, Wade D, Oram JF, Garvin M;  
 XX DR WPI; 2001-137811/14.  
 XX DR P-PSDB; AAB31367.  
 XX PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
 XX PT polynucleotides and polypeptides, useful for treatment of heart disease  
 XX PT and other disorders associated with hypercholesterolemia and  
 XX PT atherosclerosis -  
 XX PS Claim 30; Page 165-172; 211pp; English.  
 XX CC The present sequence encodes a human adenosine triphosphate (ATP)  
 XX CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
 XX CC a Tangier disease patient. ABC1 resides in cell membranes and utilizes  
 XX CC ATP hydrolysis to transport a wide variety of substrates across the  
 XX CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
 XX CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
 XX CC Tangier disease, a genetic disorder characterised by abnormal  
 XX CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
 XX CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
 XX CC pharmaceutical agents for the treatment of heart disease and other  
 XX CC disorders associated with hypercholesterolemia and atherosclerosis. The  
 XX CC genes are useful for developing screening assays to screen for compounds  
 XX CC that regulate the expression of genes associated with cholesterol  
 XX CC transport. The genes and proteins are also useful with cholesterol  
 XX CC as diagnostic indicators of cardiovascular disease and other disorders  
 XX CC associated with hypercholesterolemia.  
 XX SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;  
 Query Match 85.1%; Score 188; DB 22; Length 10474;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-86;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 34 ccgcagagccagccgaccttctccgggctgcggcaggcaggcgggagctccg 93  
 Db 42 ccgcagagccagccgaccttctccgggctgcggcaggcaggcgggagctccg 101  
 QY 94 cgcacacagagccggttctcaggcgcttgccttcttctcccggttctctgtt 153  
 Db 102 cgcacacagagccggttctcaggcgcttgccttcttctcccggttctctgtt 161  
 QY 154 tctccctctccggaagcttgcgaagggttaggagaaagagcgaacacaaagt 213  
 Db 162 tctccctctccggaagcttgcgaagggttaggagaaagagcgaacacaaagt 221  
 QY 214 gaaaaacag 221  
 Db 222 gaaaaacag 229  
 RESULT 19  
 AAS04035  
 ID AAS04035 standard; cDNA; 446 BP.  
 XX AC AAS04035;  
 XX

DT 12-SEP-2001 (first entry)  
 XX Partial human ABC1 cDNA sequence.  
 DE  
 XX  
 KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
 KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
 KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 185..438  
 FT /\*tag= a  
 FT /product= "Human ABC1 protein, amino acids 1 to 60"  
 XX  
 PN WO200130848-A2.  
 XX 03-MAY-2001.  
 PD  
 XX  
 XX 26-OCT-2000; 2000WO-EF10886.  
 PF  
 XX 26-OCT-1999; 99PP-0402668.  
 PR  
 XX 01-MAR-2000; 2000US-0186260.  
 PR  
 XX (AVET ) AVENTIS PHARMA SA.  
 PA  
 XX Denefle P, Rosier-Montus M, Arnould-Requigne I, Prades C, Naudin L;  
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
 PI Dean M;  
 XX  
 XX WPI; 2001-316327/33.  
 DR P-PSDB; AAU02176.  
 DR  
 XX New human ABC1 nucleic acids and polypeptides for treating  
 XX atherosclerosis, malaria and diabetes -  
 PT  
 XX Example 2; Page 167; 368pp; English.  
 PS  
 XX The sequence represents the partial coding sequence of human ABC1,  
 XX which encodes amino acids 1-60 of the human ABC1 protein. The nucleic  
 XX acid sequence, primers and probes derived from the ABC1 sequence, and  
 XX polypeptides and vectors are useful for the prevention of  
 XX atherosclerosis, in a subject affected by a dysfunction in the reverse  
 XX transport of cholesterol. The polypeptide encoded by the ABC1 gene is  
 XX useful for screening for an active ingredient for the prevention or  
 XX treatment of a disease resulting from dysfunction in the reverse  
 XX transport of cholesterol. The nucleic acids and polypeptides are also  
 XX useful for treating and preventing cardiovascular and neurological  
 XX pathologies, and other diseases e.g. Tangier disease, lecithin-  
 XX cholesterol (LCAT) deficiency, malaria and diabetes.  
 XX SQ Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;  
 Query Match 41.6%; Score 92; DB 22; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-37;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 130 cttgtttttcccggttctgtttctcccttctccggaagctgtcaagggttagga 189  
 Db 1 cttgtttttcccggttctgtttctcccttctccggaagctgtcaagggttagga 60  
 QY 190 gaaagagcgcgaacacacaaagtggaaacag 221  
 Db 61 gaaagagcgcgaacacacaaagtggaaacag 92  
 RESULT 20  
 AAS06120  
 ID AAS06120 standard; cDNA; 9741 BP.  
 XX AC AAS06120;  
 XX

DT 12-SEP-2001 (first entry)  
 XX Human ABC1 DNA sequence #1.  
 DE  
 XX  
 KW Human: ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
 KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
 KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 185..6967  
 FT /\*tag= a  
 FT /product= "Human ABC1 protein"  
 XX  
 XX WO200130848-A2.  
 XX  
 XX 03-MAY-2001.  
 PD  
 XX 26-OCT-2000; 2000WO-EP10886.  
 PF  
 XX 26-OCT-1999; 99EP-0402668.  
 PR  
 XX 01-MAR-2000; 2000US-0186260.  
 PR  
 XX (AVET ) AVENTIS PHARMA SA.  
 PA  
 XX Deneffe P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;  
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
 PI Dean M;  
 XX  
 DR WPI; 2001-316327/33.  
 DR P-P5DB; AAU02176.  
 XX  
 XX New human ABC1 nucleic acids and polypeptides for treating  
 PT atherosclerosis, malaria and diabetes -  
 PT  
 XX Claim 1; Page 204-208; 368pp; English.  
 PS  
 XX The sequence represents the coding sequence #1 of human ABC1. The  
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,  
 CC and polypeptides and vectors are useful for the prevention of  
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse  
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is  
 CC useful for screening for an active ingredient for the prevention or  
 CC treatment of a disease resulting from dysfunction in the reverse  
 CC transport of cholesterol. The nucleic acids and polypeptides are also  
 CC useful for treating and preventing cardiovascular and neurological  
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-  
 CC cholesterol (LCAT) deficiency, malaria and diabetes.  
 XX  
 SQ Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;

Query Match 41.6%; Score 92; DB 22; Length 9741;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-37;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 130 cttgtttttcccggttctgtttctcccttcccggaagcttgcgaagggtagga 189  
 Db 1 cttgtttttcccggttctgtttctcccttcccggaagcttgcgaagggtagga 60  
 QY 190 gaaagagacgcaaacacaaagtggaaaacag 221  
 Db 61 gaaagagacgcaaacacaaagtggaaaacag 92  
 RESULT 21  
 AAF24681  
 ID AAF24681 standard; DNA; 1643 BP.  
 XX  
 AC AAF24681;  
 XX  
 DT 20-APR-2001 (first entry)

XX Nucleotide sequence of the 5' flanking region of the human ABC1 gene.  
 DE  
 XX  
 KW Human: adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078972-A2.  
 XX  
 PD 28-DEC-2000.  
 XX  
 XX 16-JUN-2000; 2000WO-US16765.  
 PF  
 XX 18-JUN-1999; 99US-0140264.  
 PR  
 XX 14-SEP-1999; 99US-0153872.  
 PR  
 XX 19-NOV-1999; 99US-0166573.  
 XX  
 XX (CVTH-) CV THERAPEUTICS INC.  
 PA  
 XX Lawn RM, Wade D, Garvin M;  
 PI  
 XX WPI; 2001-137812/14.  
 DR  
 XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 PT useful for the development of agents for the treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX  
 PS Claim 1; Page 143-144; 215pp; English.  
 XX  
 XX The present sequence represents the 5' flanking region of the human  
 CC adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1  
 CC resides in cell membranes and utilises ATP hydrolysis to transport a wide  
 CC variety of substrates across the plasma membrane. ABC1 is a pivotal  
 CC protein in the apolipoprotein-mediated mobilisation of intracellular  
 CC cholesterol stores. ABC1 is defective in Tangier disease, a genetic  
 CC disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1  
 CC gene is localised to chromosome 9q22-q31. The ABC1 genes and proteins  
 CC are useful for developing pharmaceutical agents for the treatment of  
 CC heart disease and other disorders associated with hypercholesterolemia  
 CC and atherosclerosis. The genes are useful for developing screening assays  
 CC to screen for compounds that regulate the expression of genes associated  
 CC with cholesterol transport. The genes and proteins are also useful for  
 CC other disorders associated with hypercholesterolemia.  
 XX  
 SQ Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;

Query Match 41.2%; Score 91; DB 22; Length 1643;  
 Best Local Similarity 100.0%; Pred. No. 8e-37;  
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 gtaattgcgagcagagtgagtgaggccgagcccgagagccgagccgaccttctc 60  
 Db 1553 gtaattgcgagcagagtgagtgaggccgagcccgagagccgagccgaccttctc 1612  
 QY 61 ccgggtctcggcagggcagggcgaggagctc 91  
 Db 1613 ccgggtctcggcagggcagggcgaggagctc 1643  
 RESULT 22  
 AAF24703  
 ID AAF24703 standard; DNA; 1643 BP.  
 XX  
 AC AAF24703;  
 XX  
 DT 20-APR-2001 (first entry)



XX 15-OCT-1998.  
 PD  
 XX  
 XX 10-APR-1998; 98WO-US06955.  
 XX  
 XX 10-APR-1997; 97US-0838821.  
 XX  
 XX (GENY ) GENETICS INST INC.  
 XX  
 XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;  
 PI Racie LA, Spaulding V, Treacy M;  
 XX WPI; 1999-070077/06.  
 DR

XX New polynucleotides encoding human secreted proteins - derived from  
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,  
 PT ovary, pituitary, retina and colon cDNA libraries.  
 XX  
 XX Claim 1; Page 459; 618pp; English.

XX The present sequence represents a human expressed sequence tag (EST).  
 CC The polynucleotide, which is a secreted EST, and the encoded protein  
 CC are predicted to have useful biological activities which would make  
 CC them suitable for treating, preventing or ameliorating medical  
 CC conditions in humans and animals, although no supporting data is  
 CC given. Suggested activities include nutritional activity, immune  
 CC stimulating or suppressing activity, haematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic  
 CC activity, receptor/ligand activity, anti-inflammatory activity,  
 CC cadherin/tumour invasion suppressor activity, tumour inhibition  
 CC activity. The polynucleotide may also be useful for gene therapy.  
 XX  
 XX Sequence 447 BP; 120 A; 107 C; 95 G; 125 T; 0 other;

Query Match 8.6%; Score 19; DB 20; Length 447;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaagag 196  
 |||||  
 Db 396 caaggggtaggagaagag 414

RESULT 25  
 AAQ06308/c  
 ID AAQ06308 standard; DNA; 710 BP.  
 XX  
 XX AAQ06308;  
 AC  
 XX 29-JAN-1991 (first entry)  
 DT  
 XX

DE Sequence of DNA fragment F7 of the human IFN-gamma receptor.  
 XX  
 XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 KW  
 XX  
 XX Homo sapiens.

OS  
 XX EP393502-A.  
 PN  
 XX 24-OCT-1990.  
 PD  
 XX 11-APR-1990; 90EP-0106992.  
 XX  
 XX 19-APR-1989; 89EP-0810295.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 PA  
 XX Fountoulakis M, Garotta G, Stuber D;  
 PI  
 XX WPI; 1990-322042/43.  
 XX  
 DR

DR P-PSDB; AAR07472.  
 XX  
 XX Soluble interferon-gamma receptors - for treating auto-immune  
 PT diseases, chronic inflammations, etc.  
 PT  
 XX  
 XX Disclosure; Fig 18; 174pp; English.  
 PS  
 XX  
 XX IFN-gamma is a therapeutically active agent in the treatment  
 CC of autoimmune disease, allograft transplant rejections, multiple  
 CC sclerosis, chronic inflammations and delayed hypersensitivity. It is  
 CC also useful in identifying IFN-gamma agonists and antagonists.  
 CC See also AAQ06301.  
 XX  
 XX Sequence 710 BP; 206 A; 147 C; 166 G; 191 T; 0 other;

Query Match 8.6%; Score 19; DB 11; Length 710;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaagag 196  
 |||||  
 Db 94 CAAGGGGTAGGAGAAAGAG 76

RESULT 26  
 AAQ73229/c  
 ID AAQ73229 standard; cDNA; 735 BP.

XX  
 XX AAQ73229;  
 AC  
 XX 11-APR-1995 (first entry)  
 DT  
 XX

DE Soluble human interferon gamma receptor coding sequence.

XX  
 XX Interferon; gamma; IFN; receptor; immunoglobulin; constant domain;  
 KW light chain; heavy chain; Ig; chimeric protein; fusion protein;  
 KW autoimmune disease; chronic inflammation; allotransplant; rejection;  
 KW multiple sclerosis; fulminant hepatitis; neurological disease; AIDS;  
 KW poliovirus; Lyme disease; septicemia; treatment; therapy;  
 KW delayed type hypersensitivity; ss.

XX Homo sapiens.

XX  
 XX Location/Qualifiers  
 FH 1..735  
 FT CDS /\*tag= a  
 FT /product= Soluble interferon gamma receptor.  
 FT sig\_peptide 1..51  
 FT /\*tag= b  
 FT mat\_peptide 52..735  
 FT /\*tag= c

XX EP614981-A.  
 PN  
 XX 14-SEP-1994.  
 PD  
 XX 18-FEB-1994; 94EP-0102452.  
 XX  
 XX 05-MAR-1993; 93EP-0810170.  
 PR  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA  
 XX Dembic Z, Garotta G, Gentz R;  
 PI  
 XX WPI; 1994-281208/35.  
 DR  
 XX P-PSDB; AAR62023.  
 XX  
 XX Chimeric human interferon-gamma receptor/immunoglobulin proteins  
 PT - used to inhibit binding of interferon-gamma to its specific  
 PT receptor in the treatment of illnesses  
 XX  
 XX Disclosure; Figure 1; 29pp; English.  
 PS

XX The soluble form of the interferon (IFN) gamma receptor comprises  
 CC the whole extracellular domain of the natural receptor from the N-  
 CC terminus to the transmembrane region, lacks the cytoplasmic and  
 CC transmembrane domains of the natural receptor and specifically binds  
 CC IFN-gamma. The sequence encoding the soluble IFN-gamma receptor can  
 CC be used in constructs encoding chimeric proteins where the other  
 CC component of the chimeric protein is part or all of the constant  
 CC domain of a human immunoglobulin heavy or light chain. The  
 CC recombinant proteins can be used to inhibit IFN-gamma binding to its  
 CC specific receptor. They can be used for the treatment of  
 CC illnesses, especially autoimmune diseases, chronic inflammation,  
 CC delayed type hypersensitivity, allotransplant rejections, multiple  
 CC sclerosis, fulminant hepatitis, inflammatory neurological diseases  
 CC and neurological complications of AIDS, poliovirus infections, Lyme  
 CC disease and septicemia. The presence of the immunoglobulin  
 CC component in the chimeric protein increases the proteins half life in  
 CC vivo.  
 XX  
 SQ Sequence 735 BP; 223 A; 135 C; 170 G; 207 T; 0 other;

Query Match 8.6%; Score 19; DB 15; Length 735;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 178 caagggttaggagaaag 196  
 |||||  
 Db 28 CAAGGGGTAGGAGAAAG 10

RESULT 27  
 ID AAQ06301/c  
 XX AAQ06301 standard; DNA; 2184 BP.  
 AC AAQ06301;  
 XX  
 DT 29-JAN-1991 (first entry)  
 XX  
 DE Sequence encoding SacI/Asp7181 fragment of plasmid pBABLUE carrying  
 DE human interferon-gamma receptor gene.  
 XX

KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 KW hypersensitivity; ds.  
 XX

OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
 FT CDS 85..1551  
 FT /\*tag= a  
 XX

FN EP393502-A.  
 XX

PD 24-OCT-1990.  
 XX

PF 11-APR-1990; 90EP-0106992.  
 XX

PR 19-APR-1989; 89EP-0810295.  
 XX

PA (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX

PI Fountoulakis M, Garotta G, Stuber D;  
 XX

DR WPI; 1990-322042/43.  
 XX

DR P-PSDB; AAR07469.  
 XX

PT Soluble interferon-gamma receptors - for treating auto-immune  
 PT diseases, chronic inflammations, etc.  
 XX

PS Disclosure; Fig 1; 174pp; English.  
 XX

CC Sequence may be used to transform prokaryotic or mammalian host  
 CC cells via an expression vector, allowing production of the IFN-gamma

CC receptor in pure form.  
 CC The gene product is a therapeutically active agent in the treatment  
 CC of autoimmune disease, allograft transplant rejections, multiple  
 CC sclerosis, chronic inflammations and delayed hypersensitivity. It is  
 CC also useful in identifying IFN-gamma agonists and antagonists.  
 XX

SQ Sequence 2184 BP; 688 A; 413 C; 451 G; 632 T; 0 other;

Query Match 8.6%; Score 19; DB 11; Length 2184;  
 Best Local Similarity 100.0%; Pred. No. 4.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 178 caagggttaggagaaag 196  
 |||||  
 Db 112 CAAGGGGTAGGAGAAAG 94

RESULT 28  
 ID AAC13639/c  
 XX AAC13639 standard; CDNA; 367 BP.  
 AC AAC13639;  
 XX

DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 17714.  
 XX

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX

PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX

PF 21-FEB-2000; 2000EP-0200610.  
 XX

PR 26-FEB-1999; 99US-0123487.  
 XX

PA (GEST ) GENSET.  
 XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX

DR WPI; 2000-500381/45.  
 XX

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 1; SEQ ID 17714; 71pp + CD-ROM; English.  
 XX

CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors.  
 XX

SQ Sequence 367 BP; 88 A; 74 C; 62 G; 143 T; 0 other;

Query Match 8.1%; Score 18; DB 21; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 16;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 aacacaaagtggaaac 219  
 DB 104 AACACAAAGTGGAAC 87

RESULT 29  
 AAF58344/c  
 ID AAF58344 standard: cDNA; 710 BP.

XX AC AAF58344;  
 XX AC AAF58344;  
 XX 19-APR-2001 (first entry)  
 XX Human GTP-binding associated protein #44 coding sequence.  
 XX Human: guanosine triphosphate binding associated protein; GTP: GBAP;  
 KW Inflammation; AIDS; Addison's disease; anaemia; arteriosclerosis; asthma;  
 KW autoimmune disorder; hepatitis; multiple sclerosis; cancer; diabetes;  
 KW osteoporosis; psoriasis; ss.  
 XX Homo sapiens.  
 XX WO200105970-A2.  
 XX 25-JAN-2001.  
 XX 19-JUL-2000; 2000WO-US19698.  
 XX 19-JUL-1999; 99US-0144595.  
 XX 23-AUG-1999; 99US-0150460.  
 XX 15-OCT-1999; 99US-0159849.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Yue H, Tang YT, Bandman O, Hillman JL, Lal P, Au-Young J;  
 PI Reddy R, Yang J, Baughn MR, Lu DAM, Azimzai Y, Patterson C;  
 XX WPI: 2001-091972/10.  
 XX P-PSDB; AAB68544.  
 XX New guanosine triphosphate-binding associated proteins (GBAP) and their  
 PT encoding nucleic acids, useful for treating and/or diagnosing diseases  
 PT associated with GBAP expression, such as cancer, diabetes and asthma -  
 XX Claim 5; Page 216; 233pp; English.  
 XX The present invention relates to novel human guanosine triphosphate  
 CC (GTP)-binding associated proteins (GBAPs; AAB68501-AAB68556) and their  
 CC coding sequences (AAF58301-AAF58366). The proteins and coding sequences  
 CC of the present invention are useful for treating a variety of disorders  
 CC including inflammation, AIDS, Addison's disease, anaemia,  
 CC arteriosclerosis, asthma, autoimmune disorders, Grave's disease,  
 CC hepatitis, multiple sclerosis, cancer, diabetes, osteoporosis and  
 CC psoriasis.  
 XX Sequence 710 BP; 145 A; 290 C; 153 G; 122 T; 0 other;

Query Match 8.1%; Score 18; DB 22; Length 710;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 agagtggagtgccggg 31  
 DB 555 AGAGTCAGTGGGCGGG 538

RESULT 30  
 AAF15226/c  
 ID AAF15226 standard: cDNA; 758 BP.  
 XX

AC AAF15226;  
 XX 13-MAR-2001 (first entry)  
 DT Trichoderma reesei EST SEQ ID NO:7749.  
 XX  
 DE Multiple gene expression; filamentous fungal cell; EST;  
 XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
 KW culture condition; environmental stress; spore morphogenesis;  
 KW metabolic pathway engineering; catabolic pathway engineering; ss.  
 XX Trichoderma reesei.  
 OS WO200056762-A2.  
 XX 28-SEP-2000.  
 XX 22-MAR-2000; 2000WO-US07781.  
 XX 22-MAR-1999; 99US-0273623.  
 XX (NOVO ) NOVO NORDISK BIOTECH INC.  
 XX (NOVO ) NOVO NORDISK AS.  
 XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 XX WPI: 2000-594572/56.  
 DR Monitoring differential expression of genes in filamentous fungal cells  
 XX uses fluorescence-labeled nucleic acids isolated from the cells and a  
 XX substrate of expressed sequence tags -  
 XX Claim 89; Page 3125; 3161pp; English.

XX The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring  
 CC the global expression of genes from FF cells allows the production  
 CC potential of the microorganisms to be improved. New genes may be  
 CC discovered, possible functions of unknown open reading frames can be  
 CC identified and gene copy number variation and stability can be  
 CC monitored. The expression of genes can be used to study how FF cells  
 CC adapt to changes in culture conditions, environmental stress, spore  
 CC morphogenesis, recombination, metabolic or catabolic pathway  
 CC engineering. Using ESTs provides several advantages over genomic or  
 CC random cDNA clones including elimination of redundancy as one spot on an  
 CC array equals one gene or open reading frame, and organisation of the  
 CC microarrays based on function of the gene products to facilitate  
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
 CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and  
 CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
 CC all specifically claimed in the present invention.  
 XX Sequence 758 BP; 184 A; 168 C; 170 G; 199 T; 37 other;

Query Match 8.1%; Score 18; DB 21; Length 758;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 ttgtttttcccggttc 148  
 DB 487 TTGTTTTTCCCGGTC 470

RESULT 31

AAS60374  
ID AAS68374 standard; cDNA; 1166 BP.

XX AC AAS68374;  
XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #4178.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG04187.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity

XX PS Claim 1; SEQ ID No 4178; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1166 BP; 283 A; 299 C; 293 G; 278 T; 13 other;

Query Match 8.1%; Score 18; DB 23; Length 1166;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 gggctgcggcaggcagg 80  
|||||

Db 182 gggctgcggcaggcagg 199  
|||||

RESULT 32  
AAS72684/c

ID AAS72684 standard; cDNA; 1287 BP.

XX AC AAS72684;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #8488.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG08497.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity

XX PS Claim 1; SEQ ID No 8488; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1287 BP; 237 A; 461 C; 391 G; 198 T; 0 other;

Query Match 8.1%; Score 18; DB 23; Length 1287;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 ggcctgcggcaggcagg 81  
|||||

Db 734 GGCTGGCGCAGGCGAGG 717  
|||||

RESULT 33  
AAQ66990  
ID AAQ66990 standard; DNA; 1656 BP.

FT		/tag= a	
FT	TATA_signal	/note= "transcription start site"	
FT	1627		
FT		/tag= b	
XX			
XX	W09416057-A.		
XX			
XX	21-JUL-1994.		
PD			
XX	08-DEC-1993;	93WO-US11915.	
PF			
XX	31-DEC-1992;	92US-0999742.	
PPR			
XX	(DAND ) DANA FARBER CANCER INST INC.		
XX	Abe M, Kufe D;		
PPI			
XX	WPI; 1994-249205/30.		
DR			
XX	Isolated DF3 enhancer DNA sequence - is used to enhance		
PT	epithelium tissue-specific expression for treating carcinomas or		
PT	metabolic disorders		
PT			
XX	Disclosure; Fig 1A; 43pp; English.		
PS	The sequence represents the DF3 gene 5' flanking sequence. The DF3		
PS	enhancer can be linked to a heterologous coding sequence to		
XX	increase tissue-specific expression of the coding sequence in		
CC	the epithelium. These prods. can be used to treat carcinomas or		
CC	metabolic disorders such as phenylketonuria, cystic fibrosis,		
CC	hemophilia or emphysema. They can also be used as vaccines		
CC	against infectious organisms or can confer resistance to		
CC	the effects of a chemotherapeutic drug.		
CC	See also AAQ66989-95.		
XX			
XX	Sequence 1725 BP; 288 A; 588 C; 488 G; 361 T; 0 other;		
SQ			
	Query Match	8.1%; Score 18; DB 15; Length 1725;	
	Best Local Similarity	100.0%; Pred. No. 16;	
	Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps	
OY	49 gacccttctctcccgggc 66		
Dd	773 gacccttctctcccgggc 790		
RESULT 35			
ABAZ0286/C			
ID	ABA20286 standard; DNA; 2484 BP.		
XX			
AC	ABA20286;		
XX			
DT	23-JAN-2002 (first entry)		
XX			
DE	Human nervous system related polynucleotide SEQ ID NO 12617.		
XX			
KW	Human; nootropic; neuroprotective; cytostatic; dermatological; viral		
KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vuln		
KW	antiParkinsonian; antisickling; antianaemic; antiarthritic; cancer		
KW	antirheumatic; hepatotrophic; cerebroprotective; antiinflammatory;		
KW	antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;		
KW	antiparasitic; cardiant; immune disorder; cardiovascular disorder		
KW	neurological disease; infection; nephrotropic; gene therapy; vacci		
OS	Homo sapiens.		
XX			
PN	WC0200159063-A2.		
XX			
PD	16-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US011334.		
XX			

PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225277.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 18-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0233397.  
PR 14-SEP-2000; 2000US-0233398.  
PR 14-SEP-2000; 2000US-0233399.  
PR 14-SEP-2000; 2000US-0233400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 29-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 02-OCT-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 20-OCT-2000; 2000US-0242221.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249246.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250391.  
PR 01-DEC-2000; 2000US-0251160.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 06-DEC-2000; 2000US-0256719.  
PR 08-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
useful for preventing, diagnosing and/or treating nervous system  
cancers and metastases -

XX PS Disclosure; SEQ ID NO 12617; 1701pp + Sequence Listing; English.  
XX CC The invention relates to novel genes (ABA11004-ABA21534) and proteins  
XX CC (AB14678-AB18001) useful for preventing, treating or ameliorating  
XX CC medical conditions e.g. by protein or gene therapy. The genes are  
XX CC isolated from a range of human tissues disclosed in the specification.  
XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
XX CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
XX CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
XX CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
XX CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
XX CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
XX CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
XX CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
XX CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
XX CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
XX CC and parasitic infections.  
XX CC Note: The sequence data for this patent did not form part of the  
XX CC printed specification, but was obtained in electronic format directly  
XX CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 2484 BP; 440 A; 906 C; 734 G; 404 T; 0 other;

Query Match 8.18; Score 18; DB 22; Length 2484;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 gagtgagtgagggcgagga 32  
|||||||  
DB 2406 GAGTGAGTGGCGCGGGA 2389

RESULT 36  
ABA20287/c  
ID ABA20287 standard; DNA; 2484 BP.  
XX AC ABA20287;  
XX DT 23-JAN-2002 (first entry)  
XX DE Human nervous system related polynucleotide SEQ ID NO 13618.  
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;  
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
XX OS Homo sapiens.  
XX PN WO200159063-A2.  
XX PD 16-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US011334.  
XX PR 31-JAN-2000; 2000US-0179065.  
XX PR 04-FEB-2000; 2000US-0180628.  
XX PR 24-FEB-2000; 2000US-0184664.  
XX PR 02-MAR-2000; 2000US-0186350.  
XX PR 16-MAR-2000; 2000US-0189874.  
XX PR 17-MAR-2000; 2000US-0190076.  
XX PR 18-APR-2000; 2000US-0198123.  
XX PR 19-MAY-2000; 2000US-0205515.  
XX PR 07-JUN-2000; 2000US-0209467.  
XX PR 28-JUN-2000; 2000US-0214886.  
XX PR 30-JUN-2000; 2000US-0215135.  
XX PR 07-JUL-2000; 2000US-0216647.  
XX PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 03-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 21-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 25-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 26-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.

PR 20-OCT-2000; 2000US-0242221.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251160.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 06-DEC-2000; 2000US-0256719.  
 PR 08-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251866.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-541565/60.

PT Nucleic acids encoding 324 human nervous system antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating nervous system  
 PT cancers and metastases -

XX Disclosure; SEQ ID NO 12618; 1701pp + Sequence Listing; English.

XX The invention relates to novel genes (ABA11004-ABA21534) and proteins  
 CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (antagonists are useful  
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 2484 BP; 440 A; 906 C; 734 G; 404 T; 0 other;

Query Match 8.1%; Score 18; DB 22; Length 2484;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 gagtgaagtgaggccggga 32  
 |||||  
 Db 2406 GAGTGAGTGGCGCGGA 2389

# RESULT 37

AAZ86925/C

ID AAZ86925 standard; cDNA; 2779 BP.

XX AC AAZ86925;

XX 04-MAY-2000 (first entry)

XX Netrin-2 coding sequence.

XX Netrin-1; netrin-2; binding assay; neural axon outgrowth; diagnosis;  
 KW netrin-specific antibody; neurological disease; therapy; ss.

XX Unidentified.

XX US6017714-A.

XX 25-JAN-2000.

XX 07-JUN-1995; 95US-0482677.

XX 12-NOV-1993; 93US-0152019.

XX (REGC ) UNIV CALIFORNIA.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Serafini T, Kennedy T, Tessier-Lavigne M, Jessell T, Dodd J;  
 PI Placzek M;

XX WPI; 2000-136674/12.

XX P-PSDB; AAY76838.

XX New binding assay for identifying agents which specifically bind to  
 PT netrin proteins which can be used as diagnostic tools for neurological  
 PT diseases -

XX Disclosure; Column 17-20; 23pp; English.

XX This sequence encodes a netrin protein. The invention relates to a  
 CC binding assay using a netrin or portion of a netrin protein to identify  
 CC an agent which specifically binds a netrin. The assay comprises:  
 CC (1) contacting a prospective agent with a netrin which modulates axon  
 CC outgrowth or guidance or elicits a netrin-specific antibody; and  
 CC (2) determining if the agent specifically binds netrin. Vertebrate netrin  
 CC proteins are involved in modulating neural axon outgrowth and identifying  
 CC agents which bind or modulate netrin function allows identification of  
 CC regulators of axon outgrowth and orientation which can be used as  
 CC diagnostic reagents for neurological disease and for the development of  
 CC neurological disease therapy. Natural and synthetic chemical libraries  
 CC can be screened using these methods to identify reagents suitable for use  
 CC in human and animal clinical trials and pharmacological agents or lead  
 CC compounds for agents capable of mimicking or modulating netrin function

CC can also be identified. The methods are cost-effective, amenable to  
 CC automation and can provide high throughput screening.

XX Sequence 2779 BP; 565 A; 897 C; 797 G; 520 T; 0 other;

Query Match 8.1%; Score 18; DB 21; Length 2779;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 agtggggccgggaccgc 37  
 Db 1782 AGTGGGGCCGGGACCGC 1765

RESULT 38  
 AAQ92367/C  
 ID AAQ92367 standard; cDNA; 2783 BP.

XX AC AAQ92367;

XX AC 24-DEC-1995 (first entry)

XX DE Chick p75 cDNA.

XX KW Neural axon out-growth modulator; epidermal growth factor; EGF;  
 KW netrin-2; p75; neurodegenerative disease; transgenic animal;  
 KW gene therapy; ss.

XX OS Gallus sp.

XX FH Key Location/Qualifiers  
 FT CDS 4..1749  
 ET /\*tag= a

XX PN W09513367-A1.

XX PD 18-MAY-1995.

XX PF 08-NOV-1994; 94WO-US12913.

XX PR 12-NOV-1993; 93US-0152019.

XX PA (REGC ) UNIV CALIFORNIA.  
 XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Dodd J, Jessell T, Kennedy T, Placzek M, Serafini T;  
 XX PI Tessier-Lavigne M;

XX XX WPI; 1995-194086/25.  
 XX DR P-PSDB; AAR74187.

XX PT Neural axon out-growth modulators derived from EGF-like repeats of  
 PT netrin 1 or netrin 2 - comprise peptide(s) capable of selectively  
 PT increasing spinal axon out-growth or directing axon orientation

XX PS Disclosure; Page 46-48; 58pp; English.

XX XX An E10 chick brain cDNA library was screened with probes based on  
 CC netrin-1 (p78) or netrin-2 (p75) sequences to isolate chick p78  
 CC and p75 partial cDNA clones. Full-length clones (given in  
 CC AAQ92366-67, respectively) were subsequently obtd. by 3'RACE. cDNA  
 CC is expressed e.g. in COS or insect cells for recombinant p78 and  
 CC p75 prodn., used to breed transgenic animals, or for gene therapy.

XX SQ Sequence 2783 BP; 565 A; 897 C; 797 G; 520 T; 4 other;

Query Match 8.1%; Score 18; DB 16; Length 2783;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 agtggggccgggaccgc 37

Db 1783 AGTGGGGCCGGGACCGC 1766

RESULT 39

AAZ32011/C

XX ID AAZ32011 standard; DNA; 9248 BP.

XX AC AAZ32011;

XX DT 10-JAN-2000 (first entry)

XX DE Human METH1 related EST AB001735.

XX KW Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;  
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;  
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;  
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;  
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;  
 KW arterial-venous malformation; immune deficiency; ss.

XX OS Homo sapiens.

XX PN W09937660-A1.

XX PD 29-JUL-1999.

XX PF 22-JAN-1999; 99WO-US01313.

XX PR 23-JAN-1998; 98US-0072298.

XX PR 28-AUG-1998; 98US-0098539.

XX PA (TRUE/) IRUELA-ARISPE L.

XX PA (HAST/) HASTINGS G A.

XX PA (RUBE/) RUBEN S M.

XX PI Iruela-Arispe L, Hastings GA, Ruben SM;

XX WPI; 1999-590684/50.

XX PT New isolated metalloprotease thrombospondin polypeptides, useful for  
 XX PT treating hyperproliferative disorders, cancers or autoimmune disorders

XX PS Disclosure; Page 246-252; 457pp; English.

XX XX AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human  
 CC metalloprotease thrombospondin (METH) proteins METH1 and METH2  
 CC respectively. METH1 and METH2 have been found to be potent inhibitors of  
 CC angiogenesis both in vitro and in vivo. They can be used for treating  
 CC cancer and other disorders related to angiogenesis including abnormal  
 CC wound healing, inflammation, rheumatoid arthritis, psoriasis,  
 CC endometrial bleeding disorders, diabetic retinopathy, some forms of  
 CC macula degeneration, haemangiomas, and arterial-venous malformations.  
 CC They may be useful in treating deficiencies or disorders of the immune  
 CC system, by activating or inhibiting the proliferation, differentiation,  
 CC or mobilisation (chemotaxis) of immune cells. The etiology of these  
 CC immune deficiencies or disorders may be genetic, somatic, such as  
 CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or  
 CC toxins), or infectious. They can also be used to treat inflammatory  
 CC conditions, both chronic and acute conditions. The products can also be  
 CC used for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to  
 CC AAY49511 represent sequences given in the exemplification of the present  
 CC invention.

XX SQ Sequence 9248 BP; 2475 A; 2123 C; 2207 G; 2443 T; 0 other;

Query Match 8.1%; Score 18; DB 20; Length 9248;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74-gggcaggcgggagctc 91

DB 2223 GGGCAGGGCGGGAGCTC 2206  
 RESULT 40  
 AAC90068/C  
 ID AAC90068 standard; DNA; 9248 BP.  
 XX AAC90068;  
 AC  
 CC 19-MAR-2001 (first entry)  
 DT  
 DT  
 DT  
 DE AB001735 cDNA clone.  
 XX  
 XX METH; metalloprotease; thrombospondin; angiogenesis inhibition;  
 KW cancer therapy; benign tumour; ocular angiogenic disease;  
 KW rheumatoid arthritis; psoriasis; wound healing; endometriosis;  
 KW vasculogenesis; granulation; hypertrophic scar; nonunion fracture;  
 KW scleroderma, trachoma; vascular adhesion; myocardial angiogenesis;  
 KW coronary collateral; cerebral collateral; arteriovenous malformation;  
 KW ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint; EST;  
 KW angiofibroma; fibromuscular dysplasia; expressed sequence tag;  
 KW Crohn's disease; atherosclerosis; birth control; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX  
 PN WO200071577-A1.  
 XX  
 PD  
 PD 30-NOV-2000.  
 XX  
 XX 25-MAY-2000; 2000WO-US14462.  
 XX  
 XX 25-MAY-1999; 99US-0318208.  
 PR 20-JUL-1999; 99US-0144882.  
 PR 10-AUG-1999; 99US-0147823.  
 PR 13-AUG-1999; 99US-0373658.  
 PR 22-DEC-1999; 99US-0171503.  
 PR 22-FEB-2000; 2000US-0183792.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMK) SMITHKLINE BEECHAM CORP.  
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 PA (JONA/) JONAK Z L.  
 PA (TRUL/) TRULLI S H.  
 PA (FORN/) FORNWALD J A.  
 PA (TERK/) TERRETT J A.  
 XX  
 XX IrueLA-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH;  
 PI Fornwald JA, Terrett JA;  
 PI  
 XX WPI; 2001-025136/03.  
 DR  
 XX METH1 and METH2 polynucleotides and encoded polypeptides, used to  
 PT inhibit angiogenesis in the treatment of disorders such as cancer,  
 PT rheumatoid arthritis and psoriasis.  
 XX  
 XX Claim 7; Pages 546-552; 768pp; English.  
 PS  
 CC The present invention relates to human METH1 and METH2, (ME for  
 CC metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).  
 CC The present sequence is an expressed sequence tag (EST) for METH. METH  
 CC can be used for inhibiting angiogenesis in an individual, and for  
 CC treating cancer, benign tumours, an ocular angiogenic disease,  
 CC rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis,  
 CC vasculogenesis, granulations, hypertrophic scars, nonunion fractures,  
 CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,  
 CC coronary collaterals, cerebral collaterals, arteriovenous malformations,  
 CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,

CC fibromuscular dysplasia, wound granulation, Crohn's disease or  
 CC atherosclerosis. METH can also be used in birth control. METH can also  
 CC be used in diagnostic methods for the prognosis of cancer.  
 XX  
 SQ Sequence 9248 BP; 2475 A; 2123 C; 2207 G; 2443 T; 0 other;  
 Query Match 8.1%; Score 18; DB 22; Length 9248;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 74 gggcaggcggggagctc 91  
 |||||  
 DB 2223 GGGCAGGGCGGGAGCTC 2206  
 RESULT 41  
 ABL32987  
 ID ABL32987 standard; DNA; 17294 BP.  
 XX  
 AC ABL32987;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human immune system associated gene SEQ ID NO: 960.  
 XX  
 KW Human; immune system disease; cytosine methylation; antiasthmatic;  
 KW antiarteriosclerotic; anti-anaemic; cytostatic; neurotropic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200928-A2.  
 XX  
 XX 03-JAN-2002.  
 XX  
 XX 02-JUL-2001; 2001WO-EP07537.  
 PR 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 DR WPI; 2002-130909/17.  
 XX  
 XX Nucleic acid comprising fragment of chemically modified gene, useful  
 PT for diagnosis and treatment of diseases associated with abnormal  
 PT cytosine methylation.  
 XX  
 PS Claim 1; SEQ ID NO 960; 32pp + Sequence Listing; German.  
 XX  
 CC The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 XX  
 SQ Sequence 17294 BP; 5081 A; 203 C; 3600 G; 8410 T; 0 other;  
 Query Match 8.1%; Score 18; DB 24; Length 17294;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Sep '20 08:04:12 2002

us-09-846-456-4.oli.rng

QY 179 aagggttaggaagaag 196  
 Db 12225 aagggttaggaagaag 12242

RESULT 42

AAK70011  
 ID AAK70011 standard; DNA; 21436 BP.

XX AC AAK70011;

XX DT 06-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24823.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX KW cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

XX WO200157182-A2.

PN 09-AUG-2001.

PD 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

XX 14-AUG-2000; 2000US-0225268.

XX 14-AUG-2000; 2000US-0225270.

XX 14-AUG-2000; 2000US-0225447.

XX 14-AUG-2000; 2000US-0225757.

XX 14-AUG-2000; 2000US-0225758.

XX 14-AUG-2000; 2000US-0225759.

XX 18-AUG-2000; 2000US-0226279.

XX 22-AUG-2000; 2000US-0226681.

XX 22-AUG-2000; 2000US-0226868.

XX 22-AUG-2000; 2000US-0227182.

XX 23-AUG-2000; 2000US-0227009.

XX 30-AUG-2000; 2000US-0228924.

XX 01-SEP-2000; 2000US-0229287.

XX 01-SEP-2000; 2000US-0229343.

XX 01-SEP-2000; 2000US-0229344.

XX 01-SEP-2000; 2000US-0229345.

XX 05-SEP-2000; 2000US-0229509.

XX 05-SEP-2000; 2000US-0229513.

XX 06-SEP-2000; 2000US-0230437.

XX 06-SEP-2000; 2000US-0230438.

XX 08-SEP-2000; 2000US-0231242.

XX 08-SEP-2000; 2000US-0231243.

XX 08-SEP-2000; 2000US-0231244.

XX 08-SEP-2000; 2000US-0231245.

XX 08-SEP-2000; 2000US-0231246.

XX 08-SEP-2000; 2000US-0231247.

XX 08-SEP-2000; 2000US-0231248.

XX 08-SEP-2000; 2000US-0231249.

XX 08-SEP-2000; 2000US-0231250.

XX 08-SEP-2000; 2000US-0231251.

XX 08-SEP-2000; 2000US-0231252.

XX 08-SEP-2000; 2000US-0231253.

XX 08-SEP-2000; 2000US-0231254.

XX 08-SEP-2000; 2000US-0231255.

XX 08-SEP-2000; 2000US-0231256.

XX 08-SEP-2000; 2000US-0231257.

XX 08-SEP-2000; 2000US-0231258.

XX 08-SEP-2000; 2000US-0231259.

XX 08-SEP-2000; 2000US-0231260.

XX 08-SEP-2000; 2000US-0231261.

XX 08-SEP-2000; 2000US-0231262.

XX 08-SEP-2000; 2000US-0231263.

XX 08-SEP-2000; 2000US-0231264.

XX 08-SEP-2000; 2000US-0231265.

XX 08-SEP-2000; 2000US-0231266.

XX 08-SEP-2000; 2000US-0231267.

XX 08-SEP-2000; 2000US-0231268.

XX 08-SEP-2000; 2000US-0231269.

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 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-483426/52.  
 XX

XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating cancers and  
 PT metastasis -  
 XX

FS Disclosure; SEQ ID NO 24823; 3071pp + Sequence Listing; English.  
 XX

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patients own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) treats and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/haematopoietic-related diseases, especially  
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/haematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
 CC represent sequences used in the exemplification of the present invention.  
 XX  
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 Best Local Similarity 100.0%; Pred. No. 16;  
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 AC AAK79799;  
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 DT 07-NOV-2001 (first entry)  
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 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34611.  
 XX  
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 KW cytostatic; gene therapy; vaccine; metastasis; ds.  
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 XX  
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 XX  
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XX	(HUMA-) HUMAN GENOME SCI INC.
XX	
XX	Rosen CA, Barash SC, Ruben SM;
XX	
XX	WPT; 2001-502630/55.
XX	
PT	polynucleotides encoding digestive system antigens, useful for
PT	diagnosing, treating, preventing and/or prognosing disorders of the
PT	digestive system, particularly cancer and cancer metastases -
XX	
XX	Disclosure; SEQ ID NO 4233; 986pp; English.
XX	
CC	The present invention provides the protein and coding sequences of a
CC	number of human digestive system antigens. These can be used in the
CC	diagnosis, treatment and prevention of digestive system disorders,
CC	including cancer, Meckel's diverticulum, bacterial or parasitic
CC	infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC	ulcerative colitis. The present sequence is a genomic DNA fragment
CC	encoding a digestive system antigen of the invention.
XX	
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XX	
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QY	204 cacaaaagtggaaacaa 220
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Fri Sep 20 08:04:12 2002

us-09-846-456-4.oli.rng

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Page 30

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
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Searched: 383533 seqs, 122816752 residues

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Minimum DB seq length: 0

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3	18	8.1	1656	5 PCT-US93-11915-2	Sequence 2, Appli
4	18	8.1	1725	1 US-08-324-465-5	Sequence 5, Appli
5	18	8.1	1725	2 US-08-465-981-5	Sequence 5, Appli
6	18	8.1	1725	5 PCT-US93-11915-5	Sequence 5, Appli
C 7	18	8.1	2779	3 US-08-482-677-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1  
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; Patent No. 5565334  
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; APPLICANT: Kufe, Donald  
; APPLICANT: Abe, Miyako  
; TITLE OF INVENTION: GENE TRANSCRIPTION AND  
; TITLE OF INVENTION: IONIZING RADIATION: METHODS  
; TITLE OF INVENTION: AND COMPOSITIONS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/324,465  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/999,742  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00530/065001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1656  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-324-465-2

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 ; Sequence 2, Application US/08465981  
 ; Patent No. 5874415  
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 ; APPLICANT: Kufe, Donald  
 ; APPLICANT: Abe, Miyako  
 ; TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING  
 ; TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
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 ; COMPUTER: IBM PS/2 Model 502 or 55SX  
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 ; SOFTWARE: WordPerfect (Version 5.1)  
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 ; APPLICATION NUMBER: US/08/465,981  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/324,465  
 ; FILING DATE: October 17, 1994  
 ; APPLICATION NUMBER: 07/999,742  
 ; FILING DATE: December 31, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fraser, Janis K.  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 00530/065002  
 ; TELEPHONE: (617) 542-5070  
 ; TELEFAX: (617) 542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1656  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear

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 ; APPLICANT: Abe, Miyako  
 ; TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING  
 ; TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
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 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/11915  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/999,742  
 FILING DATE: December 31, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/DOCKET NUMBER: 00530/065W01  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1656  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 PCT-US93-11915-2

Query Match 8.1%; Score 18; DB 5; Length 1656;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 gacccttctccgggc 66  
 |||  
 Db 773 GACCCCTCTCCGGGC 790

RESULT 4  
 US-08-324-465-5  
 ; Sequence 5, Application US/08324465  
 ; Patent No. 5565334  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kufe, Donald  
 ; APPLICANT: Abe, Miyako  
 ; TITLE OF INVENTION: GENE TRANSCRIPTION AND  
 ; TITLE OF INVENTION: IONIZING RADIATION: METHODS  
 ; TITLE OF INVENTION: AND COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 502 or 55SX  
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/324,465  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/999,742

;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Fraser, Janis K.  
;; REGISTRATION NUMBER: 34,819  
;; REFERENCE/DOCKET NUMBER: 00530/065001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1725  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
US-08-324-465-5

Query Match 8.1%; Score 18; DB 1; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 gaccctctctccgggc 66  
Db 773 GACCCCTCTCTCCCGGC 790

RESULT 5  
US-08-465-981-5  
; Sequence 5, Application US/08465981  
; Patent No. 5874415  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald  
; APPLICANT: Abe, Miyako  
; TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING  
; TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,981  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/324,465  
; FILING DATE: October 17, 1994  
; APPLICATION NUMBER: 07/999,742  
; FILING DATE: December 31, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00530/065002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1725  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-465-981-5

Query Match 8.1%; Score 18; DB 2; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 gaccctctctccgggc 66  
Db 773 GACCCCTCTCTCCCGGC 790

RESULT 6  
PCT-US93-11915-5  
; Sequence 5, Application PC/TUS9311915  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald  
; APPLICANT: Abe, Miyako  
; TITLE OF INVENTION: ENHANCER SEQUENCE FOR MODULATING  
; TITLE OF INVENTION: EXPRESSION IN EPITHELIAL CELLS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/11915  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/999,742  
; FILING DATE: December 31, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00530/065W01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1725  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
PCT-US93-11915-5

Query Match 8.1%; Score 18; DB 5; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 gaccctctctccgggc 66  
Db 773 GACCCCTCTCTCCCGGC 790

RESULT 7  
US-08-482-677-5/c  
; Sequence 5, Application US/08482677  
; Patent No. 6017714  
; GENERAL INFORMATION:  
; APPLICANT: Tessier-Lavigne, Marc  
; APPLICANT: Serafini, Tito  
; APPLICANT: Kennedy, Timothy

APPLICANT: Placzek, Marysia  
APPLICANT: Jessel, Thomas  
APPLICANT: Dodd, Jane  
TITLE OF INVENTION: Netrins  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,677  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UC93-300-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2779 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-482-677-5

Query Match 8.1%; Score 18; DB 3; Length 2779;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 agtggggccgggaccgc 37  
|||||  
Db 1782 AGTGGGCGGGGACCCG 1765

RESULT 8  
US-08-152-019A-41/c  
Sequence 41, Application US/08152019A  
Patent No. 5565331  
GENERAL INFORMATION:  
APPLICANT: Tessier-Lavigne, Marc  
APPLICANT: Serafini, Tito  
APPLICANT: Kennedy, Timothy  
APPLICANT: Placzek, Marysia  
APPLICANT: Jessell, Thomas  
APPLICANT: Dodd, Jane  
TITLE OF INVENTION: NEURAL AXON OUTGROWTH MODULATORS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/152,019A  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard Aron  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-59012/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299 FHT UR  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-152-019A-41

Query Match 8.1%; Score 18; DB 1; Length 2783;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 agtggggccgggaccgc 37  
|||||  
Db 1783 AGTGGGCGGGGACCCG 1766

RESULT 9  
US-08-890-980-17  
Sequence 17, Application US/08890980  
Patent No. 5998141  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan L.  
TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, ROAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,980  
FILING DATE: 10-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MIA-005.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 544 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-890-980-17

Query Match 7.2%; Score 16; DB 2; Length 544;  
Best Local Similarity 100.0%; Pred. No. 37;

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194
    |||||
Db 208 AAGGGGTAGGAGAAAG 223

RESULT 10
US-08-890-979-17
; Sequence 17, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; TITLE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/890,979
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-7000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-890-979-17

Query Match
Best Local Similarity 100.0%; Pred. No. 37; Length 544;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194
    |||||
Db 208 AAGGGGTAGGAGAAAG 223

RESULT 11
US-09-032-894-17
; Sequence 17, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0

Query Match
Best Local Similarity 100.0%; Pred. No. 37; Length 544;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194
    |||||
Db 208 AAGGGGTAGGAGAAAG 223

RESULT 12
US-09-031-626-17
; Sequence 17, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Human
US-09-031-626-17

Query Match
Best Local Similarity 100.0%; Pred. No. 37; Length 544;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194
    |||||
Db 208 AAGGGGTAGGAGAAAG 223

RESULT 13
US-08-890-980-5
; Sequence 5, Application US/08890980
; Patent No. 5998141
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,980
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

NAME: Arnold, Beth E.  
 REGISTRATION NUMBER: 35,430  
 REFERENCE/DOCKET NUMBER: MIA-005.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-832-1000  
 TELEFAX: 617-832-7000  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1002 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-890-980-5

Query Match 7.2%; Score 16; DB 2; Length 1002;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194  
 |||||  
 DB 208 AAGGGGTAGGAGAAAG 223

RESULT 14  
 US-08-890-979-5  
 ; Sequence 5, Application US/08890979  
 ; Patent No. 6030778  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan L.  
 ; APPLICANT: Ordovas, Jose M.  
 ; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS  
 ; TITLE OF INVENTION: DISORDERS  
 ; NUMBER OF SEQUENCES: 75  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/890,979  
 ; FILING DATE: 10-JUL-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Arnold, Beth E.  
 ; REGISTRATION NUMBER: 35,430  
 ; REFERENCE/DOCKET NUMBER: MIA-005.02  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-832-1000  
 ; TELEFAX: 617-832-7000  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1002 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-890-979-5

Query Match 7.2%; Score 16; DB 3; Length 1002;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194

DB 208 AAGGGGTAGGAGAAAG 223  
 |||||

RESULT 15  
 US-09-032-894-5  
 ; Sequence 5, Application US/09032894  
 ; Patent No. 6130041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan L.  
 ; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR  
 ; FILE REFERENCE: MIA-005.03  
 ; CURRENT APPLICATION NUMBER: US/09/032,894  
 ; CURRENT FILING DATE: 1998-02-27  
 ; EARLIER APPLICATION NUMBER: 08/890,980  
 ; EARLIER FILING DATE: 1997-07-10  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1002  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-032-894-5

Query Match 7.2%; Score 16; DB 3; Length 1002;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194  
 |||||  
 DB 208 aaggggtaggagaaag 223

RESULT 16  
 US-09-032-894-95  
 ; Sequence 95, Application US/09032894  
 ; Patent No. 6130041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan L.  
 ; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR  
 ; FILE REFERENCE: MIA-005.03  
 ; CURRENT APPLICATION NUMBER: US/09/032,894  
 ; CURRENT FILING DATE: 1998-02-27  
 ; EARLIER APPLICATION NUMBER: 08/890,980  
 ; EARLIER FILING DATE: 1997-07-10  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 95  
 ; LENGTH: 1002  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-032-894-95

Query Match 7.2%; Score 16; DB 3; Length 1002;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aaggggtaggagaaag 194  
 |||||  
 DB 208 aaggggtaggagaaag 223

RESULT 17  
 US-09-031-626-5  
 ; Sequence 5, Application US/09031626  
 ; Patent No. 6228581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan L.  
 ; APPLICANT: Ordovas, Jose M.  
 ; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND  
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS

us-09-846-456-4.oli.rni

Fri Sep 20 08:04:13 2002

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; ORGANISM: Streptomyces venezuelae
; US-09-105-537-21

Query Match          7.2%: Score 16; DB 4; Length 1209;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 cccgggctgcggcagg 75
Db 1120 cccgggctgcggcagg 1135
|||||

RESULT 20
US-08-318-905-21
; Sequence 21, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 117..1436
; US-08-318-905-21

Query Match          7.2%: Score 16; DB 1; Length 1494;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 caaaagtggaacag 221
|||||

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; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Human
; US-09-031-626-5

Query Match          7.2%: Score 16; DB 4; Length 1002;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aagggttaggagaaag 194
Db 208 aagggttaggagaaag 223
|||||

RESULT 18
US-09-031-626-95
; Sequence 95, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Human
; US-09-031-626-95

Query Match          7.2%: Score 16; DB 4; Length 1002;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 aagggttaggagaaag 194
Db 208 aagggttaggagaaag 223
|||||

RESULT 19
US-09-105-537-21
; Sequence 21, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1209
; TYPE: DNA

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Db 700 CAAAAGTGGAAACAG 715

RESULT 21  
US-08-483-232-21  
; Sequence 21, Application US/08483232  
; Patent No 5656431  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,232  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5656431and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1494 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 117..1436  
US-08-483-232-21

Query Match 7.2%; Score 16; DB 1; Length 1494;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 caaaagtggaaaacag 221  
Db 700 CAAAAGTGGAAACAG 715

RESULT 22  
US-08-483-140-21  
; Sequence 21, Application US/08483140  
; Patent No. 5698403

; GENERAL INFORMATION:  
; APPLICANT: ICOS Corporation  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; TITLE OF INVENTION: Hydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,140  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 6-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 6-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5698403and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32781  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1494 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 117..1436  
US-08-483-140-21

Query Match 7.2%; Score 16; DB 1; Length 1494;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 caaaagtggaaaacag 221  
Db 700 CAAAAGTGGAAACAG 715

RESULT 23  
US-08-485-938A-21  
; Sequence 21, Application US/08485938A  
; Patent No 5847088  
; GENERAL INFORMATION:  
; APPLICANT: Cousins, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

us-09-846-456-4.oli.rni

Fri Sep 20 08:04:13 2002

```

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 117..1436
; US-08-485-938A-21

Query Match 7.2%; Score 16; DB 2; Length 1494;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 caaaagtggaaaacag 221
| | | | | | | | | | | | | | | | | |
Db 700 CAAAAGTGGAAAACAG 715

RESULT 24
US-08-910-041-21
; Sequence 21, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 117..1436
; US-08-910-041-21

Query Match 7.2%; Score 16; DB 2; Length 1494;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 caaaagtggaaaacag 221
| | | | | | | | | | | | | | | | | |
Db 700 CAAAAGTGGAAAACAG 715

RESULT 25
US-09-328-474-21
; Sequence 21, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 117..1436
; US-09-328-474-21

```

```

Query Match          7.2%; Score 16; DB 3; Length 1494;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 206 caaaagtggaaaacag 221
   |||||
Db 700 CAAAAGTGGAAAACAG 715

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```

RESULT 26
US-09-100-546-21
; Sequence 21, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6099836and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 117..1436
; US-09-100-546-21

```

```

Query Match          7.2%; Score 16; DB 3; Length 1494;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 206 caaaagtggaaaacag 221
   |||||
Db 700 CAAAAGTGGAAAACAG 715

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RESULT 27
US-09-010-715-21
; Sequence 21, Application US/09010715
; Patent No. 6146625
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993

```



RESULT 30  
PCT-US94-09752-2  
; Sequence 2, Application PC/TUS9409752  
; GENERAL INFORMATION:  
; APPLICANT: David S. Strayer and Avinash Chander  
; TITLE OF INVENTION: Compositions and Methods for  
; TARGETING: Targeting Cells and Modulating Pulmonary Surfactant Secretion  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jane Massey Licata, Esq.  
; STREET: 210 Lake Drive East, Suite 201  
; CITY: Cherry Hill  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb  
; MEDIUM TYPE: STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/09752  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/176,218  
; FILING DATE: December 30, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/114,951  
; FILING DATE: August 31, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: JEFF-0042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 779-2400  
; TELEFAX: (609) 779-8488  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1881  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
PCT-US94-09752-2

Query Match 7.2%; Score 16; DB 5; Length 1881;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 gcttgcaggggtag 187  
|||||  
Db 852 GCTTGTCAAGGGTAG 867

RESULT 31  
US-07-932-454A-2  
; Sequence 2, Application US/07932454A  
; Patent No. 5262318  
; GENERAL INFORMATION:  
; APPLICANT: GUTHRIE, ELLEN P.  
; TITLE OF INVENTION: ISOLATED DNA ENCODING THE Sphi  
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND RELATED METHODS FOR PRODUCING  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS

; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/932,454A  
; FILING DATE: 19920820  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILLIAMS, GREGORY D.  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: 42078  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEFAX: (617) 523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2692 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 703..1653  
; OTHER INFORMATION: /note= "METHYLASE GENE STARTS AT  
; POSITION 703/ENDS AT 1653. RESTRICTION  
; OTHER INFORMATION: ENDONUCLEASE STARTS AT POSITION 1703/ENDS AT 2410"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1703..2410  
US-07-932-454A-2

Query Match 7.2%; Score 16; DB 1; Length 2692;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 gtggggcggggacccg 36  
|||||  
Db 462 GTGGGCGGGACCCG 477

RESULT 32  
US-08-980-241-8/c  
; Sequence 8, Application US/08980241D  
; Patent No. 6319708  
; GENERAL INFORMATION:  
; APPLICANT: Chalfie, Martin  
; APPLICANT: Taub, James J.  
; TITLE OF INVENTION: A METHOD FOR INCREASING LIFE-SPAN  
; FILE REFERENCE: 0575/51778/JFW/JSG  
; CURRENT APPLICATION NUMBER: US/08/980,241D  
; CURRENT FILING DATE: 1997-11-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 6840  
; TYPE: DNA  
; ORGANISM: Nematodes  
; FEATURE:  
; NAME/KEY: N\_region  
; LOCATION: (2138)  
; OTHER INFORMATION: N= g, a, c or t(u)  
; NAME/KEY: N\_region  
; LOCATION: (3054)  
; OTHER INFORMATION: N= g, a, c or t(u)  
; NAME/KEY: N\_region  
; LOCATION: (3060)  
; OTHER INFORMATION: N= g, a, c or t(u)

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; NAME/KEY: N_region
; LOCATION: (3070)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (3905)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (3913)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (3917)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (4045)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (4412)..(4413)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (4416)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (4735)
; OTHER INFORMATION: N= g, a, c or t(u)
; NAME/KEY: N_region
; LOCATION: (4876)
; OTHER INFORMATION: N= g, a, c or t(u)
; US-08-980-241-8

Query Match      7.2%; Score 16; DB 4; Length 6840;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 ggagaaagagagacgcaa 202
      |||||
Db 5890 GGAGAAAGAGACGCAA 5875

RESULT 33
US-09-105-537-3
; Sequence 3, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 13613
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-3

Query Match      7.2%; Score 16; DB 4; Length 13613;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 cccgggtgcggcagg 75
      |||||
Db 1925 cccgggtgcggcagg 1940

RESULT 34
US-08-922-635-21
; Sequence 21, Application US/08922635A
; Patent No. 6033871
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6033871
; CURRENT APPLICATION NUMBER: US/08/922,635A
; CURRENT FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 08/650,766
; EARLIER FILING DATE: 1996-05-20
; EARLIER APPLICATION NUMBER: 60/012,600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 15202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-922-635-21

Query Match      7.2%; Score 16; DB 3; Length 15202;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 cttctctccggggtg 68
      |||||
Db 1370 cttctctccggggtg 1385

RESULT 35
US-09-147-236-1/c
; Sequence 1, Application US/09147236A
; Patent No. 6316251
; GENERAL INFORMATION:
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: TSUCHIDA, Takayasu
; APPLICANT: YOSHINAGA, Fumihiro
; APPLICANT: TAHARA, Naoki
; APPLICANT: HAYASHI, Takahisa
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
; FILE REFERENCE: 6537-011-0PCT
; CURRENT APPLICATION NUMBER: US/09/147,236A
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/Jp97/03633
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 16836
; TYPE: DNA
; ORGANISM: Acetobacter xylinum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (869)..(1891)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3101)..(5368)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5373)..(7778)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7784)..(11761)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11764)..(12231)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12448)..(14652)
; FEATURE:

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; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or  
; OTHER INFORMATION: c  
US-09-147-236-1

Query Match 7.2%; Score 16; DB 4; Length 16836;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 cgggctgcggcaggc 77  
|||||  
Db 14919 CGGGCTGCGCAGGC 14904

RESULT 36  
US-09-147-236-10/c  
; Sequence 10, Application US/09147236A  
; Patent No. 6316251  
; GENERAL INFORMATION:  
; APPLICANT: TONOCHI, Naoto  
; APPLICANT: TSUCHIDA, Takayasu  
; APPLICANT: YOSHINAGA, Fumihiko  
; APPLICANT: TAHARA, Naoki  
; APPLICANT: HAYASHI, Takahisa  
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE  
; FILE REFERENCE: 6537-011-OPCT  
; CURRENT APPLICATION NUMBER: US/09/147,236A  
; CURRENT FILING DATE: 1999-04-08  
; EARLIER APPLICATION NUMBER: PCT/JP97/03633  
; EARLIER FILING DATE: 1997-10-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 16836  
; TYPE: DNA  
; ORGANISM: Acetobacter xylinum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1891)...(2922)  
; FEATURE:  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence is the same as SEQ ID NO:1  
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, c, or  
; OTHER INFORMATION: t  
US-09-147-236-10

Query Match 7.2%; Score 16; DB 4; Length 16836;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 cgggctgcggcaggc 77  
|||||  
Db 14919 CGGGCTGCGCAGGC 14904

RESULT 37  
US-09-320-878-19  
; Sequence 19, Application US/09320878A  
; Patent No. 6117659  
; GENERAL INFORMATION:  
; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary C.  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 300622002120  
; CURRENT APPLICATION NUMBER: US/09/320,878A  
; CURRENT FILING DATE: 1999-05-27  
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
; EARLIER FILING DATE: 1998-08-28  
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538

; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
; EARLIER FILING DATE: 1997-04-30  
; EARLIER APPLICATION NUMBER: 60/119,139  
; EARLIER FILING DATE: 1999-02-08  
; EARLIER APPLICATION NUMBER: 60/100,880  
; EARLIER FILING DATE: 1998-09-22  
; EARLIER APPLICATION NUMBER: 60/087,080  
; EARLIER FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 38506  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-320-878-19

Query Match 7.2%; Score 16; DB 3; Length 38506;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 cccgggctgcggcagg 75  
|||||  
Db 35922 cccgggctgcggcagg 35937

RESULT 38  
US-09-049-714-1/c  
; Sequence 1, Application US/09049714  
; Patent No. 6309827  
; GENERAL INFORMATION:  
; APPLICANT: Goldstein, Andrew S.  
; APPLICANT: Bestwick, Richard K.  
; TITLE OF INVENTION: Simultaneous Collection of DNA and  
; TITLE OF INVENTION: No. 6309827-Nucleic Acid Analytes  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,714  
; FILING DATE: 27-MAR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/042,124  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 017197-002410US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-049-714-1

Fri Sep 20 08:04:13 2002

us-09-846-456-4.oli.rni

Query Match 6.8%; Score 15; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 agagagcgcaaacaca 207  
DB 18 AGAGACGCAAAACACA 4

RESULT 39  
US-08-928-465-3/c  
; Sequence 3, Application US/08928465  
; Patent No. 6204024  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Joseph  
; TITLE OF INVENTION: CCR5 RNA Transcription Based  
; TITLE OF INVENTION: Amplification Assay  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Akzo No. 6204024el Patent Department  
; STREET: 1300 Piccard Drive  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,465  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gormley, Mary E.  
; REGISTRATION NUMBER: 34,409  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-948-7400  
; TELEFAX: 301-948-9751  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA Oligonucleotide"  
; HYPOTHETICAL: NO  
; US-08-928-465-3

Query Match 6.8%; Score 15; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 agagagcgcaaacaca 207  
DB 18 AGAGACGCAAAACACA 4

RESULT 40  
US-09-481-288-2/c  
; Sequence 2, Application US/09481288  
; Patent No. 6235504  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Linqi  
; APPLICANT: Lewin, Sharon R.  
; APPLICANT: Kostrikis, Leonid  
; APPLICANT: Ho, David D.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENOMIC EQUIVALENT MARKERS AND  
; TITLE OF INVENTION: THEIR USE IN QUANTITATING CELLS AND POLYNUCLEOTIDE

; TITLE OF INVENTION: SEQUENCES THEREIN  
; FILE REFERENCE: 2378-1-001N  
; CURRENT APPLICATION NUMBER: US/09/481,288  
; CURRENT FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PRIMER  
; US-09-481-288-2

Query Match 6.8%; Score 15; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 agagagcgcaaacaca 207  
DB 17 AGAGACGCAAAACACA 3

RESULT 41  
US-08-850-049-108/C  
; Sequence 108, Application US/08850049  
; Patent No. 5965726  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: METHOD OF ELIMINATING  
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/850,049  
; FILING DATE: 02-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/050,478  
; FILING DATE: 26-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/02908  
; FILING DATE: 29-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/858,747  
; FILING DATE: 27-MAR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRIS, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2026-4006US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)758-4800  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 BASE PAIRS

TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
US-08-850-049-108

Query Match 6.8%; Score 15; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 tgcggcagggcaggg 81  
Db 23 TCGCGCAGGCAGGG 9

RESULT 42  
US-08-050-478-108/c  
; Sequence 108, Application US/08050478  
; Patent No. 5972596  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: METHOD OF ELIMINATING  
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,478  
; FILING DATE: 26-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/02908  
; FILING DATE: 29-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/858,747  
; FILING DATE: 27-MAR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRY, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2026-40060US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)758-4800  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
US-08-050-478-108

Query Match 6.8%; Score 15; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 tgcggcagggcaggg 81  
Db 23 TCGCGCAGGCAGGG 9

RESULT 43  
US-09-414-117-108/c  
; Sequence 108, Application US/09414117  
; Patent No. 6291664  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT:  
; TITLE OF INVENTION: METHOD OF ELIMINATING  
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/414,117  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/850,049  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/02908  
; FILING DATE: 29-MAR-1993  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/858,747  
; FILING DATE: 27-MAR-1992  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORRY, MARY J.  
; REGISTRATION NUMBER: 34,398  
; REFERENCE/DOCKET NUMBER: 2026-40060US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)758-4800  
; TELEFAX: (212)751-6849  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
US-09-414-117-108

Query Match 6.8%; Score 15; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 tgcggcagggcaggg 81  
Db 23 TCGCGCAGGCAGGG 9

RESULT 44  
US-09-046-247-24  
; Sequence 24, Application US/09046247  
; Patent No. 6124449  
; GENERAL INFORMATION:  
; APPLICANT: NIKOS PAGRATIS  
; APPLICANT: LARRY GOLD

us-09-846-456-4.oli.rni

Fri Sep 20 08:04:13 2002

```

; APPLICANT: Ho, David D
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENOMIC EQUIVALENT MARKERS AND
; TITLE OF INVENTION: THEIR USE IN QUANTITATING CELLS AND POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES THEREIN
; FILE REFERENCE: 2378-1-00IN
; CURRENT APPLICATION NUMBER: US/09/481,288
; CURRENT FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-481-288-1

Query Match      6.8%; Score 15; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 agagacgcaaacaca 207
    |||||
Db 17 AGAGACGCAAAACACA 3

Search completed: September 20, 2002, 06:15:34
Job time: 11153 sec

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; TITLE OF INVENTION: HIGH AFFINITY TGF? NUCLEIC
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,247
; FILING DATE: 23-MARCH-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,424
; FILING DATE: 2-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX 34.2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F modified
US-09-046-247-24

```

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Query Match      6.8%; Score 15; DB 3; Length 51;
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 146 ttctgtttttcccc 160
    ::l:::lllll
Db 22 UUCUGUUUUUCCCCC 36

```

```

RESULT 45
US-09-481-288-1/c
; Sequence 1, Application US/09481288
; Patent No. 6235504
; GENERAL INFORMATION:
; APPLICANT: Zhang, Linqi
; APPLICANT: Lewin, Sharon R
; APPLICANT: Kostrikis, Leonidios

```



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 04:07:24 ; Search time 3900.56 Seconds  
(without alignments)  
764.718 Million cell updates/sec

Title: US-09-846-456-4  
Perfect score: 221  
Sequence: 1 gtaattgcagcagagtgta.....aacacaaaagtgaacacacg 221

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_estl.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_gss.\*
- 13: em\_gss\_hum.\*
- 14: em\_gss\_inv.\*
- 15: em\_gss\_pln.\*
- 16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	99.1	763	9 AU121731	AU121731 AU121731
2	217	98.2	736	9 AU135588	AU135588 AU135588
3	154	69.7	292	10 Z44377	Z44377 HSC12B081 n
4	98	44.3	998	10 BG678861	BG678861 602824760
5	30	13.6	535	10 BG384217	BG384217 303216 MA
6	21	9.5	679	12 AG037352	AG037352 Pan trogl
7	21	9.5	710	12 BH502182	BH502182 BOGH04TR
8	20	9.0	265	9 BB862540	BB862540 BB862540
9	20	9.0	389	10 BG629097	BG629097 cc-esf1cl
10	20	9.0	426	10 BG629091	BG629091 cc-esf1cl
11	20	9.0	777	10 BG123629	BG123629 EST469275
12	19	8.6	87	9 AU076672	AU076672 AU076672
13	19	8.6	300	9 AU099072	AU099072 AU099072
14	19	8.6	389	10 BI772330	BI772330 603056038
15	19	8.6	484	9 AW642780	AW642780 cm2e02.w
16	19	8.6	486	10 T78163	T78163 yd79b06.r1
17	19	8.6	530	10 BG702824	BG702824 602684727

C 18	19	8.6	554	9	AL597062	AL597062 DKF2P313C
C 19	19	8.6	597	10	BI548754	BI548754 603189147
C 20	19	8.6	609	10	BI523553	BI523553 603175746
C 21	19	8.6	616	10	BG714492	BG714492 602670936
C 22	19	8.6	656	10	BG776309	BG776309 602663377
C 23	19	8.6	664	10	BM311005	BM311005 1959e10.Y
C 24	19	8.6	674	10	BI561894	BI561894 603255765
C 25	19	8.6	686	10	BI545327	BI545327 603187458
C 26	19	8.6	688	10	BI549570	BI549570 603192272
C 27	19	8.6	694	10	BJ044199	BJ044199 BJ044199
C 28	19	8.6	703	10	BJ052576	BJ052576 BJ052576
C 29	19	8.6	704	9	AL554654	AL554654 AL554654
C 30	19	8.6	706	10	BG431399	BG431399 602500027
C 31	19	8.6	725	9	AL600963	AL600963 DKF2P313B
C 32	19	8.6	730	10	BE973918	BE973918 601880234
C 33	19	8.6	731	10	BI824845	BI824845 603033758
C 34	19	8.6	748	10	BG564438	BG564438 602584384
C 35	19	8.6	751	9	AL601135	AL601135 DKF2P313C
C 36	19	8.6	756	10	BI088379	BI088379 602851164
C 37	19	8.6	757	10	BG706900	BG706900 602672070
C 38	19	8.6	781	9	AU143746	AU143746 AU143746
C 39	19	8.6	784	10	BI458234	BI458234 603199174
C 40	19	8.6	795	10	BG705539	BG705539 602668716
C 41	19	8.6	803	10	BI548062	BI548062 603196572
C 42	19	8.6	813	9	AL542978	AL542978 AL542978
C 43	19	8.6	824	10	BG402101	BG402101 602465634
C 44	19	8.6	848	10	BI600654	BI600654 603247539
C 45	19	8.6	879	10	BI764049	BI764049 603043255

ALIGNMENTS

RESULT 1

AU121731  
LOCUS AU121731 MAMMAL Homo sapiens CDNA clone MAMMAL000851 5', mRNA  
DEFINITION AU121731 sequence.  
ACCESSION AU121731 763 bp mRNA linear EST 19-OCT-2000  
VERSION AU121731.1 GI:10936966  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 763)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.  
HRI human cDNA project  
JOURNAL Unpublished (2000)  
COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5' - & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
Location/Qualifiers  
1. .763  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="MAMMAL000851"  
/clone\_lib="MAMMAL"  
/tissue\_type="mammary gland"  
/note="Vector: pME18SF13"

TITLE  
JOURNAL  
COMMENT

FEATURES  
Source

BASE COUNT 137 a 205 c 260 g 158 t 3 others  
ORIGIN

D<sub>b</sub>  
Q<sub>y</sub>  
D<sub>b</sub>

[illegible]

ACCESSION  
Z44311  
844277 1  
GI:573506

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VERSION
Z443777.1
EST

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**KEYWORDS:** human.

SOURCE	ORGANISM	Homo sapiens	Metazoa:
1			
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Eukaryota; Metazoa;  
Eukaryota; Eutheria;  
Mammalia

----- 1 (bases 1 to 292)

REFERENCE  
AUTHORS

**Duprat, S., M.D.,** Duprat, S., M.D., Mariad

Mitchell, H., Mariani-Kabaktch

TMAGE: molecular i

TIME and its expression

JOURNAL  
C. R. Acad. Sci. I  
0557534

**MEDLINE**  
95277334  
contact: Genethon

COMMENT

Genethon Centre de

```

Db 61 CAGGGCGGGAGCTCCGGCACCACAGAGCGGTTCTCAGGGCGCTTTGCTCCTTGT 120
QY 137 ttctcccggttctgtttctcccttccggaagctgttcaaggggtagagaagag 196
|||||
Db 121 TTTCCCGGTTCTGTTTCTCCCTTNTCCGGAAGCTGTGCAAGGGGTAGGAAAGAG 180
QY 197 acgcaaacacaaaagtgaataacag 221
|||||
Db 181 ACGCAACACAAAAGTGGAAAACAG 205

RESULT 4
BG678861
LOCUS
DEFINITION
602624760f1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749735 5',
mRNA sequence.
ACCESSION
BG678861
VERSION
BG678861.1 GI:13910258
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 998)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10603 row: g column: 16
High quality sequence stop: 860.
FEATURES
source
1..998
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4749735"
/tissue_type="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: skin; Vector: PCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT
285 a 233 c 244 g 236 t
ORIGIN

Query Match 44.3%; Score 98; DB 10; Length 998;
Best Local Similarity 100.0%; Pred. No. 2.7e-39;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ttgctctgtttttcccggttctgttttcccttccggaagctgttcaagg 183
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Db 105 TTGCTCTGTGTTTCCCGGTTCTGTTTCTCCCTTCTCCGGAAGCTTGTCAAGGG 164
QY 184 gtaggagaagagacgcaacacaaaagtgaataacag 221
|||||
Db 165 GTAGGAGAAAGAGACGCAACACAAAAGTGGAAAACAG 202

RESULT 5
BG384217
LOCUS
DEFINITION
303216 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION
BG384217
VERSION
BG384217.1 GI:13308689

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KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 535)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keelle,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
EST discovery (2000)
Unpublished
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCAGTCACGACG
Plate: 90 row: G column: 13
Seq primer: ATTAGGTGACACTATAG.
FEATURES
source
Location/Qualifiers
1..535
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: PCMV SPORT6; Site:1: XbaI; Site:2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT
121 a 159 c 136 g 119 t
ORIGIN

Query Match 13.6%; Score 30; DB 10; Length 535;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 aagagacgcaacacaaaagtggaaaacag 221
|||||
Db 151 AAGAGACGCAACACAAAAGTGGAAAACAG 180

RESULT 6
AG037352/c
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-013J06.R, genomic survey sequence.
ACCESSION
AG037352
VERSION
AG037352.1 GI:16564225
KEYWORDS
GSS; GSS (genome survey sequence).
SOURCE
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-013J06.R.
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 679)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

```

Fri Sep 20 08:04:14 2002

(E-mail:chimbos@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

PRIMERS  
Sequencing: M13Rev

LIBRARY  
Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI

Location/Qualifiers

1. .679  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-013J06.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"  
22 t

BASE COUNT  
ORIGIN

Query Match 9.5% Score 21; DB 12; Length 679;  
Best Local Similarity 100.0%; Pred. NO. 4.7; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 0

Qy 146 tctgttttccccctctcc 166  
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Db 431 TTCGTTTTCCTCCCTCC 411

RESULT 7  
BH502182 710 bp DNA linear GSS 13-DEC-2001  
LOCUS BOGHN04TR BOGH Brassica oleracea genomic clone BOGHN04, DNA  
DEFINITION sequence.

ACCESSION BH502182  
VERSION BH502182.1 GI:17710279  
KEYWORDS GSS.  
SOURCE Brassica oleracea.

ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 710)  
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished (2001)  
Other\_GSSs: BOGHN04TF  
Contact: Chris Town

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.

FEATURES  
source  
1. .710  
/organism="Brassica oleracea"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone="BOGHN04"  
/note="vector: PHOS1; Site 1: BstXI; 2-3 kb sheared  
genomic DNA inserted into PHOS1 using BstXI linkers"  
177 a 196 c 128 g 209 t

BASE COUNT  
ORIGIN

Query Match 9.5% Score 21; DB 12; Length 710;

Best Local Similarity 100.0%; Pred. NO. 4.7; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 0

Qy 134 tttttccccggttctgttt 154  
|||||

Db 532 TTTTTCCTCCGCTCTGTTT 552

RESULT 8

BH862540 265 bp mRNA linear EST 26-NOV-2001  
LOCUS BH862540 RIKEN full-length enriched, brain CRL-1443 BC3H1 CDNA Mus  
DEFINITION musculus cDNA clone G430028E10 5', mRNA sequence.

ACCESSION BH862540  
VERSION BH862540.1 GI:17103994  
KEYWORDS house mouse.  
SOURCE Mus musculus

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 265)  
Akimura, T., Arakawa, T., Hiraoka, T., Hirozane, T., Imotani, K., Ishii  
Hayatsu, N., Hiramoto, K., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,  
Y., Ito, M., Kawai, J., K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,  
Nakamura, M., Nishi, K., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,  
Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa  
Shibata, K., Takaku, Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,  
A., Takahashi, F., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Watabiki, A., Muramatsu, M., Inoue, Y., Kira, A. and  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.

2001)  
Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

EMAIL: genome-res@sc.riken.go.jp/  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Muramatsu, M. and Hayashizaki, Y.  
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.

FEATURES  
source  
1. .265  
/organism="Mus musculus"  
/strain="C3H"  
/db\_xref="taxon:10090"  
/clone="G430028E10"  
/clone\_lib="RIKEN full-length enriched, brain CRL-1443  
BC3H1 CDNA"  
/tissue\_type="brain"  
/cell\_line="CRL-1443 BC3H1"  
45 a 73 c 114 g 33 t

BASE COUNT  
ORIGIN

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SOURCE
ORGANISM
tomato
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
1 (bases 1 to 426)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rvl9@cornell.edu
3 prime sequence.

FEATURES
Location/Qualifiers
1..426
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cc-esfLcLEL25011a1"
/clone_lib="tomato flower library from a mixture of
developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XL0LR"
/note="Vector: pBK.CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cLEL)."
BASE COUNT 77 a 108 c 79 g 162 t
ORIGIN

Query Match 9.0%; Score 20; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ttgtcctgtgtttttcccc 143
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DB 246 TTGCTCTCTGTTTTCCTCC 265

RESULT 11
BGI23629/c 777 bp mRNA linear EST 31-JAN-2001
LOCUS EST469275 tomato shoot/meristem Lycopersicon esculentum cDNA clone
DEFINITION CT0F2H15 5' sequence, mRNA sequence.
ACCESSION BGI23629
VERSION BGI23629.1 GI:12623817
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
1 (bases 1 to 777)
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1..777
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"

SOURCE
source

SOURCE
ORGANISM
tomato
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
1 (bases 1 to 389)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rvl9@cornell.edu
3 prime sequence.

FEATURES
Location/Qualifiers
1..389
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cc-esfLcLEL25023d1"
/clone_lib="Tomato flower library from a mixture of
developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XL0LR"
/note="Vector: pBK.CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cLEL)."
BASE COUNT 68 a 100 c 71 g 150 t
ORIGIN

Query Match 9.0%; Score 20; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ttgtcctgtgtttttcccc 143
|||||
DB 246 TTGCTCTCTGTTTTCCTCC 265

RESULT 10
BGI29091 426 bp mRNA linear EST 19-APR-2001
LOCUS cc-esfLcLEL25011a1 Tomato flower library from a mixture of
DEFINITION developmental stages Lycopersicon esculentum cDNA clone
cc-esfLcLEL25011a1, mRNA sequence.
ACCESSION BGI29091
VERSION BGI29091.1 GI:13680564
KEYWORDS EST.

SOURCE
source

SOURCE
ORGANISM
tomato
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
1 (bases 1 to 389)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rvl9@cornell.edu
3 prime sequence.

FEATURES
Location/Qualifiers
1..389
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cc-esfLcLEL25023d1"
/clone_lib="Tomato flower library from a mixture of
developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XL0LR"
/note="Vector: pBK.CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cLEL)."
BASE COUNT 68 a 100 c 71 g 150 t
ORIGIN

Query Match 9.0%; Score 20; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ttgtcctgtgtttttcccc 143
|||||
DB 246 TTGCTCTCTGTTTTCCTCC 265

RESULT 10
BGI29091 426 bp mRNA linear EST 19-APR-2001
LOCUS cc-esfLcLEL25011a1 Tomato flower library from a mixture of
DEFINITION developmental stages Lycopersicon esculentum cDNA clone
cc-esfLcLEL25011a1, mRNA sequence.
ACCESSION BGI29091
VERSION BGI29091.1 GI:13680564
KEYWORDS EST.

SOURCE
source

SOURCE
ORGANISM
tomato
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
1 (bases 1 to 426)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rvl9@cornell.edu
3 prime sequence.

FEATURES
Location/Qualifiers
1..426
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cc-esfLcLEL25011a1"
/clone_lib="tomato flower library from a mixture of
developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XL0LR"
/note="Vector: pBK.CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cLEL)."
BASE COUNT 77 a 108 c 79 g 162 t
ORIGIN

Query Match 9.0%; Score 20; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ttgtcctgtgtttttcccc 143
|||||
DB 246 TTGCTCTCTGTTTTCCTCC 265

RESULT 11
BGI23629/c 777 bp mRNA linear EST 31-JAN-2001
LOCUS EST469275 tomato shoot/meristem Lycopersicon esculentum cDNA clone
DEFINITION CT0F2H15 5' sequence, mRNA sequence.
ACCESSION BGI23629
VERSION BGI23629.1 GI:12623817
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
1 (bases 1 to 777)
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1..777
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"

SOURCE
source

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```

/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Small greenhouse leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
BASE COUNT      262 a 143 c 210 g 162 t
ORIGIN

Query Match      9.0%; Score 20; DB 10; Length 777;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ttgctctgtttttcccc 143
      |||||||
Db 495 TTGCTCTGTTTTCCTCC 476

RESULT 12
AU076672/c
LOCUS
DEFINITION
AU076672 Sugano cDNA library Homo sapiens cDNA clone HEP02824
similar to 5'-end region of Human interferon-gamma receptor mRNA,
mRNA sequence.
ACCESSION
AU076672
VERSION
AU076672.1 GI:7439153
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 87)
AUTHORS
Suzuki,Y., Ishihara,D., Sasaki,M., Nakagawa,H., Hata,H., Tsunoda,T.,
Watanabe,M., Komatsu,T., Ota,T., Isogai,T., Suyama,A. and Sugano
,S.
TITLE
Statistical analysis of the 5' untranslated region of human mRNA
using 'Oligo-Capped' cDNA libraries
JOURNAL
Genomics 64 (3), 286-297 (2000)
MEDLINE
20221373
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997)
This clone was obtained from a 'full length-enriched' cDNA library
constructed by 'Oligo-capping' method. The coding region starts
from the 50 bp upstream to the 3'-end.
FEATURES
source
Location/Qualifiers
1..87
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP02824"
/clone_lib="Sugano cDNA library"
BASE COUNT      11 a 27 c 28 g 21 t
ORIGIN

Query Match      8.6%; Score 19; DB 9; Length 87;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaaag 196
      |||||||
Db 65 CAAGGGTAGGAGAAAG 47

RESULT 14
BI772330/c
LOCUS
DEFINITION
BI772330 389 bp mRNA linear EST 25-SEP-2001
603056038F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205633 5',
mRNA sequence.
ACCESSION
BI772330
VERSION
BI772330.1 GI:15763908
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 389)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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RESULT 13
AU099072/c
LOCUS
DEFINITION
AU099072 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP16514 similar to Human interferon-gamma receptor mRNA, mRNA
sequence.
ACCESSION
AU099072
VERSION
AU099072.1 GI:13550201
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 300)
AUTHORS
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
,K., Suyama,A. and Sugano,S.
TITLE
In silico mapping of the 5'-ends of human mRNAs using full-length
enriched and 5'-end enriched cDNA libraries constructed by
Oligo-capping method
JOURNAL
Unpublished (2001)
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
Location/Qualifiers
1..300
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP16514"
/clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT      62 a 76 c 87 g 75 t
ORIGIN

Query Match      8.6%; Score 19; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaaag 196
      |||||||
Db 116 CAAGGGTAGGAGAAAG 98

RESULT 14
BI772330/c
LOCUS
DEFINITION
BI772330 389 bp mRNA linear EST 25-SEP-2001
603056038F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205633 5',
mRNA sequence.
ACCESSION
BI772330
VERSION
BI772330.1 GI:15763908
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 389)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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Plate: LLAM11515 row: k column: 10
High quality sequence stop: 389.
FEATURES
  source
    1...389
    Location/Qualifiers
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:5205633"
      /lab_host="NIH_MGC_122"
      /lab_host="DH10B"
      /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
      Site_1: NotI; Site_2: EcoRI (destroyed); RNA source
      anonymous pool of 24 week female lung, 16 week female
      spleen, and 20-22 week male spleens. Library is oligo-dT
      primed and directionally cloned (EcoRI site is destroyed
      upon cloning). Average insert size 1.4 kb, insert size
      range 1-3 kb. Library is normalized and enriched for
      full-length clones and was constructed by C. Gruber
      (Invitrogen). Research Genetics tracking code 026. Note:
      this is a NIH_MGC Library."
BASE COUNT      96 a  91 c  93 g  109 t
ORIGIN
Query Match      8.6%; Score 19; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggtaggagaagag 196
      |||||
Db 60 CAAGGGTAGGAGAAGAG 42

RESULT 15
AW642780
LOCUS
DEFINITION
  cm22e02.w1 Blackshear/Soares normalized Xenopus egg library Xenopus
  laevis cDNA clone PBX0121E02 5', mRNA sequence.
ACCESSION
  AW642780
VERSION
  AW642780.1 GI:7400093
KEYWORDS
  EST.
SOURCE
  African clawed frog.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
  Xenopodinae; Xenopus.
REFERENCE
  1 (bases 1 to 484)
  Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.
  Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman
  , J.W., Bonaldo, M.F. and Soares, M.B.
  The NIEHS Xenopus maternal EST project: interim analysis of the
  first 13,879 ESTs from unfertilized eggs
Gene 267 (1), 71-87 (2001)
21211403
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
cdna@resgen.com
DNA Sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).
PCR Primers
FORWARD: TGTAACGACGGCCAGT
BACKWARD: CAGGAACGCTATGACC
Plate: 0121 row: E column: 02
Seq primer: T7 primer.
Location/Qualifiers

1...486
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="PBX0121E02"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/note="Vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI;
polyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dn18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT73-Pac vector.
The library contained approximately 7.2 X 10^5
recombinants, with average insert sizes of 1-1.5 kb."
BASE COUNT      120 a  83 c  110 g  171 t
ORIGIN
Query Match      8.6%; Score 19; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 ctcaggggcgcttgcctc 131
      |||||
Db 345 CTCAGGGCGCTTGTCTCT 363

RESULT 16
T78163
LOCUS
DEFINITION
  Yd79b06.r1 Soares fetal liver spleen INFIS Homo sapiens cDNA clone
  IMAGE:114419 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR
  ALPHA CHAIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
  T78163
VERSION
  T78163.1 GI:696672
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 486)
  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
  , M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
  Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston
  , R., Williamson, A., Wohldmann, P. and Wilson, R.
  The WashU-Werck EST Project
Unpublished (1995)
Other ESTs: yd79b06.s1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert size: 1053
High quality sequence stops: 475
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1053 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 475.
Location/Qualifiers

1...486
/organism="Homo sapiens"

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cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National

cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National

cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 597)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM11636 row: n column: 12

High quality sequence stop: 593.

FEATURES source  
Location/Qualifiers  
1..597  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5260619"  
/clone\_lib="NIH\_MGC\_95"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site: 1: BamHI; Site: 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to 500 ng. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI), National Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 163 a 124 c 150 g 160 t

ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 597;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaaag 196  
|||||

DB 91 CAAGGGGTAGGAGAAAG 73

RESULT 20  
BI523553 609 bp mRNA linear EST 29-AUG-2001  
LOCUS 603175746P1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5240195',  
DEFINITION mRNA sequence.

ACCESSION BI523553

VERSION BI523553.1 GI:15348345

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 609)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM11605 row: k column: 12

High quality sequence start: 31

High quality sequence stop: 608.

## FEATURES source

Location/Qualifiers  
1..609  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5240195"  
/clone\_lib="NIH\_MGC\_121"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH\_MGC Library."

BASE COUNT 184 a 120 c 143 g 162 t

ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 609;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaaag 196  
|||||

DB 59 CAAGGGGTAGGAGAAAG 41  
|||||

## RESULT 21

LOCUS BG714492/c 616 bp mRNA linear EST 08-MAY-2001  
DEFINITION 602670936F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4793528 5',  
mRNA sequence.

ACCESSION BG714492

VERSION BG714492.1 GI:13993423

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 616)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM10673 row: h column: 09

High quality sequence stop: 616.

Location/Qualifiers

1..616

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4793528"

/clone\_lib="NIH\_MGC\_96"

/tissue\_type="hypothalamus"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 182 a 123 c 150 g 161 t

Query Match 8.6%; Score 19; DB 10; Length 616;  
Best Local Similarity 100.0%; Pred. No. 49;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 caagggttaggagaagag 196  
|||||

Db 68 CAAGGGGTAGGAGAGAG 50

RESULT 22  
BG776309/c

LOCUS 656 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602663377F1 NIH\_MGC\_59 Homo sapiens cDNA clone IMAGE:4608562 5',  
mRNA sequence.

ACCESSION BG776309

VERSION BG776309.1 GI:14046626

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 656)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [csapbs-remail.nih.gov](mailto:csapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LCM1661 row: j column: 19

High quality sequence stop: 656.

Location/Qualifiers

1..656

/organism="Homo sapiens"

/db.xref="taxon:9606"

/clone="IMAGE:4608562"

/clone\_lib="NIH\_MGC\_59"

/tissue\_type="mucoepidermoid carcinoma"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site\_1:

SfiI (ggcgctggcc); Site\_2: SfiI (ggccattggcc);

Double-stranded cDNA was prepared from cell line RNA.

5' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor

sequence: 5'-AFTCTAGAGCGAGCGCGGACATG-dT(30)AN-3'

(where B = A, C, G, or T). Average

insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC

Library."

BASE COUNT 189 a 134 c 160 g 173 t

Query Match 8.6%; Score 19; DB 10; Length 656;

Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 caagggttaggagaagag 196  
|||||

Db 60 CAAGGGGTAGGAGAGAG 42

RESULT 23  
BM311005/c

LOCUS 664 bp mRNA linear EST 03-JAN-2002

DEFINITION 1959e10.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:INGR\_HUMAN  
PI260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR ;, mRNA  
sequence.

ACCESSION BM311005

VERSION BM311005.1 GI:18045350

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 664)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas

, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R., Williams, T.

, Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: [dmelton@biohp.harvard.edu](mailto:dmelton@biohp.harvard.edu)

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

([hino@im.wustl.edu](mailto:hino@im.wustl.edu))

Seq primer: -40RP from Gibco

High quality sequence stop: 485.

Location/Qualifiers

1..664

/organism="Homo sapiens"

/db.xref="taxon:9606"

/clone\_lib="HR85 islet"

/tissue\_type="Purified pancreatic islet"

/lab\_host="DH10B"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:

NotI; Site\_2: XhoI; cDNA made by oligo-dr priming.

Size-selected on agarose gel. Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD,

Metabolism Div. (Alan Permutt Lab), Washington University

School of Medicine, Box 8127, 660 South Euclid Ave., St.

Louis, MO 63110, E-mail: [hino@im.wustl.edu](mailto:hino@im.wustl.edu), Tel:

314-362-1916, Fax: 314-747-2692."

BASE COUNT 194 a 134 c 157 g 179 t

Query Match 8.6%; Score 19; DB 10; Length 664;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 caagggttaggagaagag 196  
|||||

Db 53 CAAGGGGTAGGAGAGAG 35

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L16M11652 row: c column: 16  
High quality sequence stop: 568.

FEATURES  
source

1. .686  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5258823"  
/clone\_lib="NIH\_MGC\_95"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcagag  
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
size-selected for average insert size 2.5 kb and  
normalized to ROT 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIH/NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT  
ORIGIN

188 a 152 c 170 g 176 t

Query Match 8.6%; Score 19; DB 10; Length 686;

Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaagag 196  
|||||

Db 91 CAAGGGGTAGGAGAAGAG 73  
|||||

RESULT 26

BI549570  
LOCUS BI549570 688 bp mRNA linear EST 05-SEP-2001  
DEFINITION 603192272F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5263721 5',  
mRNA sequence.

ACCESSION BI549570

VERSION BI549570.1 GI:15436882

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 688)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L16M11664 row: o column: 18

High quality sequence stop: 688.

Location/Qualifiers

1. .688

/organism="Homo sapiens"

RESULT 24

BI561894/c

LOCUS BI561894

DEFINITION 603255765F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:5297945 5',

mRNA sequence.

ACCESSION BI561894

VERSION BI561894.1 GI:15449208

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 674)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L16M11754 row: a column: 18

High quality sequence stop: 674.

Location/Qualifiers

1. .674

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5297945"

/clone\_lib="NIH\_MGC\_97"

/lab\_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcagag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',

size-selected for average insert size 2.2 kb and

normalized to ROT 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH\_MGC Library."

192 a 139 c 166 g 177 t

Query Match 8.6%; Score 19; DB 10; Length 674;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaagag 196  
|||||

Db 74 CAAGGGGTAGGAGAAGAG 56  
|||||

RESULT 25

BI545327/c

LOCUS BI545327

DEFINITION 603187458F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5258823 5',

mRNA sequence.

ACCESSION BI545327

VERSION BI545327.1 GI:15432639

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

/db\_xref="taxon:9606"  
 /clone="IMAGE:5263721"  
 /clone\_lib="NIH\_MGC\_95"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH108"  
 /note="Organ: brain; Vector: pBluescriptR (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcag  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',  
 size-selected for average insert size 2.5 kb and  
 normalized to R0T 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NIMH/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library."  
 149 a 221 c 218 g 100 t

BASE COUNT  
 ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 688;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggaagaag 196  
 |||||

Db 456 CAAGGGCTAGGAGAAAG 474

RESULT 27  
 BJ044199/c

LOCUS  
 DEFINITION BJ044199 NIBB Mochii normalized Xenopus neurula library EST 06-DEC-2001  
 laevis cDNA clone XL012122 3', mRNA sequence.

ACCESSION BJ044199

VERSION BJ044199.1 GI:17397688

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 694)

Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara

, Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1. .694

/organism="Xenopus laevis"

/db\_xref="taxon:9606"

/clone="XL012122"

/clone\_lib="NIBB Mochii normalized Xenopus neurula

library"

/tissue\_type="whole embryo"

/dev\_stage="stage 15"

230 a 129 c 119 g 216 t

BASE COUNT

ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 694;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 ctacggcgctttgctct 131

|||||

Db 632 CTCAGGCGCTTTCCTCT 614

RESULT 28  
 BJ052576/c

LOCUS

DEFINITION BJ052576 NIBB Mochii normalized Xenopus neurula library EST 11-DEC-2001

laevis cDNA clone XL041019 3', mRNA sequence.

ACCESSION BJ052576

VERSION BJ052576.1 GI:17498622

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 703)

Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara

, Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1. .703

/organism="Xenopus laevis"

/db\_xref="taxon:9606"

/clone="XL041019"

/clone\_lib="NIBB Mochii normalized Xenopus neurula

library"

/tissue\_type="whole embryo"

/dev\_stage="stage 15"

235 a 129 c 122 g 217 t

BASE COUNT

ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 703;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 ctacggcgctttgctct 131

|||||

Db 644 CTCAGGCGCTTTCCTCT 626

RESULT 29  
 AL554654/c

LOCUS

DEFINITION AL554654 LTI\_NFL006.PL2 Homo sapiens cDNA clone CS0DI085YJ06 5

prime, mRNA sequence.

ACCESSION AL554654

VERSION AL554654.1 GI:12895644

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 704)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .704

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DI085YJ06"

/clone.lib="LFI\_NFL006\_PL2"  
 /tissue\_type="placenta"  
 /note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com  
 BASE COUNT 204 a 132 c 169 g 191 t 8 others  
 ORIGIN

Query Match 8.6%; Score 19; DB 9; Length 704;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggttaggagaaag 196  
 ||||||||||||||||  
 Db 59 CAAGGGGTAGGAGAAAG 41

RESULT 30  
 BG431399/c 706 bp mRNA linear EST 14-MAR-2001  
 LOCUS 602500027F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4613742 5',  
 DEFINITION mRNA sequence.  
 ACCSSION BG431399  
 VERSION BG431399.1 GI:13337905  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 706)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: crabs-r@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCMI364 row: e column: 07  
 High quality sequence stop: 701.  
 Location/Qualifiers  
 1..706  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4613742"  
 /clone\_lib="NIH\_MGC\_75"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: kidney; Vector: pDNR-LiB (Clontech); Site\_1: SfiI (ggccctcgcc); Site\_2: SfiI (ggccattagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGCGCGGCGCGCATG-dh(30)BN-3' (where B = A, C, G or T). Average insert size 1.65 Kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

BASE COUNT 212 a 131 c 166 g 197 t  
 ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 178 caaggggttaggagaaag 196  
 ||||||||||||||||  
 Db 26 CAAGGGGTAGGAGAAAG 8  
 RESULT 31  
 AL600963/c 725 bp mRNA linear EST 14-AUG-2001  
 LOCUS DKFZp313B0639\_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone  
 DEFINITION DKFZp313B0639 5', mRNA sequence.  
 ACCESSION AL600963  
 VERSION AL600963.1 GI:15164469  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 725)  
 Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
 Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
 EST (Duesterhoeft, et al.)  
 Unpublished (1999)  
 Contact: Duesterhoeft A  
 MIPS Am Klopferstr. 18a D-82152 Martinsried, Germany  
 This is the 5' sequence of the clone insert  
 clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.  
 No SI sequence available.  
 This clone (DKFZp313B0639) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
 Location/Qualifiers  
 1..725  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="DKFZp313B0639"  
 /clone\_lib="313 (Synonym: hlcc2)"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiI; cDNA-collection"  
 BASE COUNT 206 a 141 c 174 g 193 t 11 others  
 ORIGIN

Query Match 8.6%; Score 19; DB 9; Length 725;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 178 caaggggttaggagaaag 196  
 ||||||||||||||||  
 Db 62 CAAGGGGTAGGAGAAAG 44  
 RESULT 32  
 BE973918/c 730 bp mRNA linear EST 04-OCT-2000  
 LOCUS BE973918 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:3950528 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BE973918  
 VERSION BE973918.1 GI:10587254  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BASE COUNT 206 a 141 c 174 g 193 t 11 others  
 ORIGIN

```

REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-remail.nih.gov
             Tissue Procurement: CLONETECH Laboratories, Inc.
             CDNA Library Preparation: CLONETECH Laboratories, Inc.
             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM817 row: c column: 09
             High quality sequence stop: 577.
             Location/Qualifiers
               1..730
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:3950528"
                 /lab_host="NIH_MGC_83"
                 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                 Site_1: SfII (ggcgctcgcc); Site_2: SfII (ggcattagggc
                 ); 5' and 3' adaptors were used in cloning as follows: 5'
                 adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
                 sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3',
                 (where B = A, C, G or T). Average
                 insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
                 contained inserts by PCR. This library was enriched for
                 full-length clones and was constructed by Clontech
                 Laboratories (Palo Alto, CA)."
BASE COUNT   203 a 155 c 184 g 188 t
ORIGIN
Query Match      8.6%; Score 19; DB 10; Length 730;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggtaggagaaag 196
|||||
DB 91 CAAGGGTAGGAGAAGAG 73

RESULT 33
BI824845/c
LOCUS
DEFINITION      731 bp mRNA linear EST 04-OCT-2001
                 603033758F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174751 5',
                 mRNA sequence.
ACCESSION      BI824845
VERSION
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-remail.nih.gov
             CDNA Library Preparation: CLONETECH Laboratories, Inc.
             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1553 row: g column: 22
             High quality sequence stop: 709.
             Location/Qualifiers
               1..748
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:4712109"
                 /lab_host="NIH_MGC_76"
                 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
                 SfII (ggcgctcgcc); Site_2: SfII (ggcattagggc); 5' and
                 3' adaptors were used in cloning as follows: 5' adaptor
                 sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
                 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A,
                 C, G or T). Average insert size 1.85
                 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
                 by PCR. This library was enriched for full-length clones
                 and was constructed by Clontech Laboratories (Palo Alto,
                 CA). Note: this is a NIH_MGC Library."
FEATURES
source
1..731
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5174751"
/lab_host="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT   216 a 143 c 173 g 199 t
ORIGIN
Query Match      8.6%; Score 19; DB 10; Length 731;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggtaggagaaag 196
|||||
DB 50 CAAGGGTAGGAGAAGAG 32

RESULT 34
BG564438/c
LOCUS
DEFINITION      748 bp mRNA linear EST 10-APR-2001
                 602584384F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4712109 5',
                 mRNA sequence.
ACCESSION      BG564438
VERSION
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-remail.nih.gov
             CDNA Library Preparation: CLONETECH Laboratories, Inc.
             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1553 row: g column: 22
             High quality sequence stop: 709.
             Location/Qualifiers
               1..748
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:4712109"
                 /lab_host="NIH_MGC_76"
                 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
                 SfII (ggcgctcgcc); Site_2: SfII (ggcattagggc); 5' and
                 3' adaptors were used in cloning as follows: 5' adaptor
                 sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
                 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A,
                 C, G or T). Average insert size 1.85
                 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
                 by PCR. This library was enriched for full-length clones
                 and was constructed by Clontech Laboratories (Palo Alto,
                 CA). Note: this is a NIH_MGC Library."
FEATURES
source

```

```
BASE COUNT      215 a      146 c      184 g      203 t
ORIGIN

Query Match      8.6%; Score 19; DB 10; Length 748;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaag 196
|||||
Db 60 CAAGGGGTAGGAGAAGAG 42

RESULT 35
AL601135/c
LOCUS
DEFINITION DKF2p31302239_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION AL601135
VERSION DKF2p31302239 5', mRNA sequence.
KEYWORDS EST.
SOURCE AL601135.1 GI:15164641
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 751)
AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann
, S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Duesterhoeft A
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
researched by Olagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No SI sequence available.
This clone (DKF2p31302239) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..751
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p31302239"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI;
cDNA-collection"
BASE COUNT      207 a      147 c      188 g      203 t      6 others
ORIGIN

Query Match      8.6%; Score 19; DB 9; Length 751;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaag 196
|||||
Db 87 CAAGGGGTAGGAGAAGAG 69

RESULT 36
BI088379/c
LOCUS
DEFINITION 602851164F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4992998 5',
mRNA sequence.
ACCESSION BI088379
VERSION BI088379.1 GI:14506709
KEYWORDS EST.
```

```
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1012 row: o column: 15
High quality sequence stop: 660.
FEATURES
Location/Qualifiers
1..756
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4992998"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT      216 a      154 c      193 g      193 t
ORIGIN

Query Match      8.6%; Score 19; DB 10; Length 756;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caagggttaggagaag 196
|||||
Db 107 CAAGGGGTAGGAGAAGAG 89

RESULT 37
BG706900/c
LOCUS
DEFINITION 602672070F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4794785 5',
mRNA sequence.
ACCESSION BG706900
VERSION BG706900.1 GI:13982706
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10676 row: l column: 18
High quality sequence stop: 757.
FEATURES
Location/Qualifiers
```

```

source
1..757
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4794785"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothenamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      206 a 157 c 197 g 197 t
ORIGIN

Query Match      8.6%; Score 19; DB 10; Length 757;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaaagag 196
|||||
DB 111 CAAGGGGTAGGAGAAAGAG 93

RESULT 38
AUI43746 781 bp mRNA linear EST 25-OCT-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 781)
AUTHORS
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isogai, T.
TITLE
HRI human cDNA project
JOURNAL
Unpublished (2000)
COMMENT
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
1..781
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Y79AA1002429"
/clone_lib="Y79AA1"
/cell_type="retinoblastoma"
/cell_line="Y79"
/note="Vector: pME18SFL3"
BASE COUNT      225 a 156 c 190 g 207 t 3 others
ORIGIN

Query Match      8.6%; Score 19; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaaagag 196
|||||
DB 111 CAAGGGGTAGGAGAAAGAG 93

RESULT 38
AUI43746 781 bp mRNA linear EST 25-OCT-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 781)
AUTHORS
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isogai, T.
TITLE
HRI human cDNA project
JOURNAL
Unpublished (2000)
COMMENT
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
1..781
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5278435"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothenamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      214 a 159 c 212 g 198 t 1 others
ORIGIN

Query Match      8.6%; Score 19; DB 10; Length 784;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaaagag 196
|||||
DB 136 CAAGGGGTAGGAGAAAGAG 118

RESULT 40
BG705539/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
EST.

```



## ORIGIN

Query Match 8.6%; Score 19; DB 9; Length 813;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaaag 196  
|||||

DB 62 CAAGGGGTAGGAGAAAG 44

## RESULT 43

BG402101/c

DEFINITION 60245634F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4593728 5',  
mRNA sequence.

ACCESSION BG402101

VERSION BG402101.1 GI:13295549

KEYWORDS EST.

SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 824)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM1334 row: c column: 09

High quality sequence stop: 569.

Location/Qualifiers

1. 824

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4593728"

/clone\_lib="NIH\_MGC\_75"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site\_1:

Sfil (ggcgcctggcc); Site\_2: Sfil (ggcattatggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCCATATGCCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCCGAGCGGCCGACATG-DT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.65

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH\_MGC Library."

BASE COUNT 214 a 186 c 223 g 201 t

ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 824;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaaag 196

|||||

DB 100 CAAGGGGTAGGAGAAAG 82

## RESULT 44

BG402101/c

LOCUS

DEFINITION 603247539F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5299400 5',

mRNA sequence.

ACCESSION BI600654

VERSION 603247539F1

KEYWORDS EST

SOURCE human

## ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 848)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11757 row: n column: 09

High quality sequence stop: 686.

Location/Qualifiers

1. 848

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5299400"

/clone\_lib="NIH\_MGC\_96"

/tissue\_type="hypothalamus"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag



size-selected for average insert size 2.3 kb and

normalized to R0T 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 216 a 199 c 205 g 228 t

ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 848;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaaag 196

|||||

DB 68 CAAGGGGTAGGAGAAAG 50

## RESULT 45

BI764049/c

LOCUS

DEFINITION 603043255F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5183797 5',

mRNA sequence.

ACCESSION BI764049

VERSION BI764049.1 GI:15755627

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 879)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11458 Row: m Column: 14  
 High quality sequence stop: 829.  
 Location/Qualifiers  
 1. .879  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5183797"  
 /clone\_lib="NIH\_MGC\_116"  
 /lab\_host="DH10B"  
 /note="Organ: pooled colon, kidney, stomach; Vector:  
 PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 023. Note: this is a NIH\_MGC Library."

BASE COUNT 254 a 175 c 198 g 252 t  
 ORIGIN

Query Match 8.6%; Score 19; DB 10; Length 879;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 caaggggtaggagaaag 196  
 |||||  
 Db 45 CAAGGGTAGGAGAAAGAG 27

Search completed: September 20, 2002, 04:07:29  
 Job time: 13783 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 06:32:15 ; Search time 5250.46 Seconds  
(without alignments)  
633.720 Million cell updates/sec

Title: US-09-846-456-5  
Perfect score: 159  
Sequence: 1 ttaatgaccagccacggcg.....cttccagaagaagaaca 159

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Lasting first 45 summaries

Database :

GenEmbl:\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	159	100.0	159	6	AX351033	Sequence
2	159	100.0	357	6	AX351030	Sequence
3	77	48.4	10442	6	AX060713	Sequence
4	77	48.4	10442	6	AX060892	Sequence
5	77	48.4	10442	6	AF285167	Homo sapi
6	77	48.4	10474	6	AX060719	Sequence
7	77	48.4	10474	6	AX060721	Sequence
8	77	48.4	10474	6	AX060898	Sequence
9	77	48.4	10474	6	AX060900	Sequence
10	77	48.4	149034	9	AF275948	Homo sapi
11	60	37.7	200	9	AF258623s2	Homo sapi
12	60	37.7	298	9	AB037924	Homo sapi
13	60	37.7	446	6	AX127764	Sequence
14	60	37.7	446	6	AX139751	Sequence
15	60	37.7	480	9	HS252277	Homo sapi
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26	60	37.7	129608	9	AL353685	Human DNA
27	60	37.7	175064	2	AC012230	Homo sapi
28	60	37.7	183999	6	AX092589	Sequence
29	60	37.7	201144	9	AF287262	Homo sapi
30	51	32.1	1556	9	AK024328	Homo sapi
31	44	27.7	90698	2	AC021345	Homo sapi
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34	21	13.2	21	6	AX092707	Sequence
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40	19	11.9	684	6	AR074136	Sequence
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## ALIGNMENTS

RESULT	1	AX351033	Sequence 5 from Patent WO0183746.	159 bp	DNA	linear	PAT 06-FEB-2002
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DEFINITION	AX351033	Sequence 5 from Patent WO0183746.					
ACCESSION	AX351033	Sequence 5 from Patent WO0183746.					
VERSION	AX351033.1	GI:18616389					
KEYWORDS	human.						
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	1 (sites)						
AUTHORS	Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.						
TITLE	Regulatory nucleic acid sequences of the abcl gene						
JOURNAL	Patent: WO 0183746-A 5 08-NOV-2001;						
FEATURES	Avantis Pharma S.A. (FR)						
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ORIGIN							

AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Lawn, R.M., Wade, D. and Garvin, M.  
Regulation with binding cassette transporter protein abcl  
Patent: WO 0078972-A 1 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)

BASE COUNT	2898 a	2297 c	2408 g	2835 t	4 others
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DEFINITION Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
complete cds.
ACCESSION AF285167
VERSION AF285167.1 GI:9755158
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Schwartz, K., Lawn, R.M., and Wade, D.P.
TITLE ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 10442)
AUTHORS Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Selthamer, J.J., Vaughan, A.M., and Oram, J.F.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
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DEFINITION Sequence 7 from Patent WO0078972.
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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DEFINITION Sequence 9 from Patent WO0078972.
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KEYWORDS human.
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	Lawn, R.M., Wade, D. and Garvin, M.									
TITLE	Regulation with binding cassette transporter protein abcl1									
JOURNAL	Patent: WO 0078972-A 9 28-DEC-2000;									
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AUTHORS	Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.									
TITLE	Atp binding cassette transporter protein abcl1 polypeptides									
JOURNAL	Patent: WO 0078971-A 7 28-DEC-2000;									
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41657..41679
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Query Match 48.4%; Score 77; DB 9; Length 149034;  
 Best Local Similarity 99.2%; Pred. No. 2e-32;  
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 agctgtgccctcctccagggtccgagccacacgctggcgctgctgagggga 91  
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 QY 92 acatggcatgttgccctcagctgaggtgtgctgtggaagaacctcacttcagaagaa 151  
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 Db 25922 ACATGCTGTGTGGCTCAGCTGAGGTGTGCTGTGGAAGAACCCTCATTTCAGAGAA 25981  
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 QY 152 gacaaaca 159  
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 Db 25982 GACAAACA 25989

RESULT 11  
 AF25862352  
 LOCUS AF25862352 200 bp DNA linear PRI 23-JUN-2000  
 DEFINITION Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene, exon 2.

ACCESSION AF258624  
 VERSION AF258624.1 GI:7769714

KEYWORDS 2 of 4  
 SEGMENT human.  
 SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Pullinger,C.K., Hakamata,H., Duchateau,P.N., Eng,C.,

Aouizerat,B.E., Fielding,C.J. and Kane,J.P.

TITLE Analysis of hABCI gene 5' end: additional peptide sequence.

JOURNAL promoter region, and four polymorphisms

REFERENCE Biochem. Biophys. Res. Commun. 271 (2000) In press

AUTHORS 2 (bases 1 to 200)

Aouizerat,B.E., Hakamata,H., Duchateau,P.N., Eng,C.,

Fielding,C.J. and Kane,J.P.

TITLE Direct Submission

JOURNAL Submitted (23-JUN-2000) Cardiovascular Research Institute,

University of California, San Francisco, 505 Parnassus Avenue, San

Francisco, CA 94143-0130, USA

REMARK Sequence update by submitter

FEATURES Location/Qualifiers

1..200

/organism="Homo sapiens"

exon  
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 /chromosome="9"  
 /map="9q31"  
 22..179  
 /gene="ABCA1"  
 /number=2  
 37 a 57 g 50 t  
 BASE COUNT  
 ORIGIN

Query Match 37.7%; Score 60; DB 9; Length 200;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tgttgccctcagctgaggtgtgctgtggaagaacctcacttcagaagaacaaaca 159  
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 Db 120 TGTGGCCTCAGCTGAGGTGTGCTGTGGAAGAACCCTCATTTCAGAGAACAACA 179  
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RESULT 12  
 AB037924

LOCUS AB037924 298 bp mRNA linear PRI 12-OCT-2000  
 DEFINITION Homo sapiens mRNA for ABC1, partial cds.  
 ACCESSION AB037924  
 VERSION AB037924.1 GI:9711458  
 KEYWORDS ABC1.  
 SOURCE Homo sapiens placenta cDNA to mRNA.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Zhao,L.X., Zhou,C.J., Tanaka,A., Nakata,M., Hirabayashi,T.,

Amachi,T., Shioda,S., Ueda,K. and Inagaki,N.

TITLE Cloning, characterization and tissue distribution of the rat

JOURNAL ATP-binding cassette (ABC) transporter ABC2/ABCA2

REFERENCE Biochem. J. 350 (Pt 3), 865-872 (2000)

2 (bases 1 to 298)

Ueda,K., Kioka,N. and Tanaka,A.

Direct Submission

TITLE Submitted (02-FEB-2000) Kazumitsu Ueda, Kyoto University Graduate

School of Agriculture, Division of Applied Life Sciences;

Kitashirakawa, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

(E-mail:uedak@kais.kyoto-u.ac.jp, Tel:81-75-753-6105,

Fax:81-75-753-6104)

FEATURES Location/Qualifiers

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/db\_xref="taxon:9606"

/tissue\_type="placenta"

88..298

/gene="ABCA1"

88..>298

/gene="ABCA1"

/codon\_start=1

/product="ABC1"

/protein\_id="BAB07875.1"

/db\_xref="GI:9711459"

/translation="MACWPQLRLILWKNLTFRRQTCLLEAVPLFLLILISVRL

SYPPYEQHECHFPNKAMPAGTLPW"

BASE COUNT 60 a 87 c 77 g 72 t 2 others

ORIGIN

Query Match 37.7%; Score 60; DB 9; Length 298;

Best Local Similarity 100.0%; Pred. No. 9.8e-23;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tgttgccctcagctgaggtgtgctgtggaagaacctcacttcagaagaacaaaca 159  
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 Db 94 TGTGGCCTCAGCTGAGGTGTGCTGTGGAAGAACCCTCATTTCAGAGAACAACA 153  
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RESULT 13  
 LOCUS AX127764 446 bp DNA linear PAT 15-MAY-2001  
 DEFINITION Sequence 3 from Patent WO0130848.  
 ACCESSION AX127764  
 VERSION AX127764.1 GI:14134411  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,  
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,  
 Remaley, A., Brewer, H.B. and Dean, M.  
 TITLE Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: WO 0130848-A 3 03-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
 Location/Qualifiers  
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 /organism="synthetic construct"  
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 /note="Oligonucleotide Primer"  
 BASE COUNT 96 a 123 c 112 g 115 t  
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Query Match 37.7%; Score 60; DB 6; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 100 ttgtgacctcagctaggtctgtgtggaagacctcactttcagaagaagacaaca 159  
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 Db 191 TGTGGCCTCAGCTAGGTTGCTGTGTGGAAGAACCTCACTTTCAGAGAAGACAACA 250

RESULT 14  
 LOCUS AX139751 446 bp DNA linear PAT 30-MAY-2001  
 DEFINITION Sequence 3 from Patent EP1096012.  
 ACCESSION AX139751  
 VERSION AX139751.1 GI:14275333  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,  
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,  
 Remaley, A., Brewer, H.B. and Dean, M.  
 TITLE Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: EP 1096012-A 3 02-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
 Location/Qualifiers  
 source  
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 BASE COUNT 96 a 123 c 112 g 115 t  
 ORIGIN

Query Match 37.7%; Score 60; DB 6; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 15

HSA252277  
 LOCUS Homo sapiens partial ABC-1 gene for ATP-binding cassette transporter-1, exon 2.  
 DEFINITION  
 ACCESSION AJ252277  
 VERSION AJ252277.1 GI:12140344  
 KEYWORDS ABC-1 gene; ATP-binding cassette transporter-1.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 480)  
 AUTHORS Porsch-Oezcuereomez, M., Langmann, T. and Schmitz, G.  
 TITLE Cloning and Characterization of the human ATP-binding Cassette  
 Transporter-1 (ABC-1) Promoter  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 480)  
 AUTHORS Porsch-Oezcuereomez, M.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-JAN-2000) Porsch-Oezcuereomez M.K., Institute for  
 Clinical Chemistry, University of Regensburg,  
 Franz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY  
 FEATURES  
 Location/Qualifiers  
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 189..346  
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 281..346  
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 /function="cholesterol efflux regulatory protein"  
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 /protein\_id="CAC21428.1"  
 /db\_xref="GI:12140345"  
 /translation="MACWPQLRLWLKNTFRERRQT"  
 BASE COUNT 89 a 102 c 155 g 134 t  
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 Query Match 37.7%; Score 60; DB 9; Length 480;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 100 ttgtgacctcagctaggtctgtgtggaagacctcactttcagaagaagacaaca 159  
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 Db 287 TGTGGCCTCAGCTAGGTTGCTGTGTGGAAGAACCTCACTTTCAGAGAAGACAACA 346  
 RESULT 16  
 LOCUS AF258627 697 bp mRNA linear PRI 11-MAY-2000  
 DEFINITION Homo sapiens ATP binding cassette transporter 1 (ABCA1) mRNA,  
 partial cds.  
 ACCESSION AF258627  
 VERSION AF258627.1 GI:7769707  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 697)  
 AUTHORS Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,  
 Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

**TITLE** Analysis of hABC1 gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

**JOURNAL** Biochem. Biophys. Res. Commun. 271 (2000) In press

**REFERENCE** 2 (bases 1 to 697)

**AUTHORS** Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

**TITLE** Direct Submission

**JOURNAL** Submitted (19-APR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA

**FEATURES** Location/Qualifiers

**source** 1..697

**gene** 1..>697

**CDS** 396..>697

**ORIGIN** 152 a 198 c 190 g 156 t 1 others

**Query Match** 37.7%; Score 60; DB 9; Length 697;

**Best Local Similarity** 100.0%; Pred. No. 9.5e-23;

**Matches** 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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**Db** 402 TGTGGCCTCAGCTGAGTGTGCTGTGGAAGACCTCATTTCAGAGAAGACAACA 461  
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**RESULT 17**

**AB055982** 1 GI:15212106

**LOCUS** AB055982 Homo sapiens mRNA for ABCA1, complete cds. linear PRI 18-AUG-2001

**DEFINITION** Homo sapiens mRNA for ABCA1, complete cds.

**ACCESSION** AB055982

**VERSION** AB055982.1

**KEYWORDS** Homo sapiens cDNA to mRNA.

**SOURCE** Homo sapiens

**ORGANISM** Homo sapiens

**REFERENCE** 1 (bases 1 to 6786)

**AUTHORS** Tanaka, A.R., Abe-Dohmae, S., Arakawa, R., Sadanami, K., Kidera, A., Kioka, N., Amachi, T., Yokoyama, S. and Ueda, K.

**TITLE** A new topological model of functional human ABCA1-Signal peptide cleavage and glycosylation of a large extracellular domain

**JOURNAL** Unpublished

**REFERENCE** 2 (bases 1 to 6786)

**AUTHORS** Ueda, K., Kioka, N. and Tanaka, A.R.

**TITLE** Direct Submission

**JOURNAL** Submitted (20-FEB-2001) Kazumitsu Ueda, Kyoto University Graduate School, Applied Life Sciences; Kitashirakawa, Kyoto Sakyo-ku, Kyoto 606-8502, Japan (E-mail: uedak@kais.kyoto-u.ac.jp, Tel:81-75-753-6105, Fax:81-75-753-6104)

**FEATURES** Location/Qualifiers

**Source** 1..6786

**gene** 1..6786

**CDS** 1..6786

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/product="ABCA1"

/protein\_id="BAB63210.1"

/db\_xref="GI:15212107"

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NLSLPKSTVDKMLRADVILHKVFLQGVQLHSLCNGSEEMIQGLDQSVSLGCLP  
REKLAARFVLRNMDILKPLRLASTSPFSKELAEATKLLHSLGTLAQELFSMR  
SWDMRQEVMLPFRNNSSTQIYQAVSRIVCGHGGGLKIKSLNWDNNYKALF  
GGNGDEAETFYDNTSTPYCNDLKNLSPSLRIIWKALKPLLVKILYLPDTPAT  
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QQLDGLDWTADQIVAFVAKHPEDVQSSNGSVYTRAFENPHTQAIIRTSFMECVNLN  
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EQIGVQMDNLFESPEEDGNLTYSVMMLFTFLYGVNTWYIEAVFGYQIGPRPW  
YFCTKSYWFEESDEKSHPGSNQKRISEICMEEPTHLKLGVSIGNLVKRYRGMKV  
AVDGLALNFYGOITSLFHNGAGKTTTMSILTGLPPTSGTAYILGKDIRSEMSTIR  
ONLGVCPQHNVLDFMLTVEEHIWYFARLKLSEKHVKAEMQNALDGLVPSKLSKT  
SOLSGGNQRLVALAFVGSKVILDEPTAGVDYPSRRGIWELLKLYRGRITLIST  
HMDAEDVLGDRITAIISHGKCCVGSFLKQNLQGTGYLTLVKDKVSSLSRNS  
STVSYLKKESSVQSSDAGLSDHSDTLTIDVSAISNLIRKHVSEARLVEDIGHL  
TYVLPYAAKEGAFVELFDRLSDIGTSSYIGISITTEELFLKVAESGVDAETS  
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TTAPVPTIMDLFONGNWTQNPSPCCSSDKIKMLPVCPPGAGLPPQRKNQTA  
DILQDLTGRNISDLYLVKTYQIIAKSLKNIWNEFRYGGFSLGVSNTQALPPSQEVN  
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NAILRANLQKGNPSHYGIFAFNPLNLTKQOLSEVALMTTSDVLVSIIPAMSFV  
PASFPVPLIOERYSKAKHLOFISGVKPIVWLSNFVMDMNVVVPATLVITIIIFCQO  
KSVYSNLPVLALLLLLYGWSITPLMYPASVFEKIPSTAYVVLTVTSNLFINGNSVA  
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PLSDWLVGRNLFAMAVEGVFFLITLYQYRFFIRPRPVNAKSLPLNDEDEDVRRERO  
RIIDGGGNDILEIKELTKYRRRKPADVRCIGIPPGCEGFLGNGAGKSGSTFKM  
LTGDTVTVRGDAFLNLSILNTHVHONGYCPQDAITELTGRHEVFEFALLRGV  
PERVGVKGEWAIKRLGLVKYGEKYNKSGNKRKLSTAMALIGGPPVPLVDPTTG  
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**BASE COUNT** 1724 a 1643 c 1759 g 1660 t

**ORIGIN**

**Query Match** 37.7%; Score 60; DB 9; Length 6786;

**Best Local Similarity** 100.0%; Pred. No. 8.8e-23;

**Matches** 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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**Db** 7 TGTGGCCTCAGCTGAGTGTGCTGTGGAAGAACCTCATTTCAGAGAAGACAACA 66  
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**RESULT 18**

**AB053452** 1 GI:16073979

**LOCUS** AB053452 Homo sapiens

**DEFINITION** Sequence 3 from Patent WO0170810.

**ACCESSION** AB053452

**VERSION** AB053452.1

**KEYWORDS** human.

**SOURCE** Homo sapiens

**ORGANISM** Homo sapiens

**REFERENCE** 1 (bases 1 to 7260)

**AUTHORS** Schmitz, G. and Bodzioch, M.

**TITLE** Atp binding cassette transporter 1 (abcl1) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid,

JOURNAL  
 Patent: WO 0170810-A 3 27-SEP-2001;  
 Bayer Aktiengesellschaft (DE)  
 FEATURES  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

BASE COUNT 1834 a 1765 c 1905 g 1756 t  
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 8.8e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 327 TGTGGCCTCAGCTGAGGTGCTGCTGTGGAAGAACCTCAGTTTCAGAGAAGACAAACA 386

RESULT 19  
 LOCUS AX092594 7860 bp DNA linear PAT 21-MAR-2001  
 DEFINITION Sequence 6 from Patent WO0115676.  
 ACCESSION AX092594  
 VERSION AX092594.1 GI:13444651  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 7860)  
 Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.  
 Compositions and methods for modulating hdl cholesterol and  
 triglyceride levels  
 JOURNAL Patent: WO 0115676-A 6 08-MAR-2001;  
 University of British Columbia (CA); Xenon Genetics Inc. (CA)  
 FEATURES  
 Location/Qualifiers  
 source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

BASE COUNT 2014 a 1860 c 2008 g 1978 t  
 ORIGIN

Query Match 37.7%; Score 60; DB 6; Length 7860;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tttggcctcagctgaggttgcctgtggaagaacacctcactttcagaagaagacaaaca 159  
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 Db 81 TGTGGCCTCAGCTGAGGTGCTGCTGTGGAAGAACCTCAGTTTCAGAGAAGACAAACA 140

RESULT 20  
 LOCUS AX135712 7862 bp DNA linear PAT 29-MAY-2001  
 DEFINITION Sequence 1 from Patent WO0132184.  
 ACCESSION AX135712  
 VERSION AX135712.1 GI:14271961  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 7862)  
 Attie, A.D., Cook, M., Gray-Keller, M.P., Hayden, M.R., Pimstone, S. and  
 Brooks-Wilson, A.  
 Abcl modulation for the modulation of cholesterol transport  
 JOURNAL Patent: WO 0132184-A 1 10-MAY-2001;  
 WISCONSIN ALUMNI RESEARCH FOUNDATION (US)  
 FEATURES  
 Location/Qualifiers  
 source  
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BASE COUNT 2014 a 1860 c 2008 g 1978 t  
 ORIGIN

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 2013 a 1861 c 2010 g 1978 t  
 ORIGIN

Query Match 37.7%; Score 60; DB 6; Length 7862;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tttggcctcagctgaggttgcctgtggaagaacacctcactttcagaagaagacaaaca 159  
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 Db 81 TGTGGCCTCAGCTGAGGTGCTGCTGTGGAAGAACCTCAGTTTCAGAGAAGACAAACA 140

RESULT 21  
 LOCUS AX127830 9741 bp DNA linear PAT 15-MAY-2001  
 DEFINITION Sequence 69 from Patent WO0130848.  
 ACCESSION AX127830  
 VERSION AX127830.1 GI:14134477  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 9741)  
 Deneffe, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,  
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,  
 Remaley, A., Brewer, H.B. and Dean, M.  
 Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: WO 0130848-A 69 03-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others  
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 Best Local Similarity 100.0%; Pred. No. 8.7e-23;  
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 DEFINITION Sequence 69 from Patent EP1096012.  
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 VERSION AX139817.1 GI:14275399  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 9741)  
 Deneffe, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,  
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,  
 Remaley, A., Brewer, H.B. and Dean, M.  
 Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: EP 1096012-A 69 02-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
 Location/Qualifiers  
 source  
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 /organism="Homo sapiens"

BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others  
 ORIGIN

Query Match 37.7%; Score 60; DB 6; Length 9741;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-23;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tttggcctcagctgaggttgcctgtggaagaacacctcactttcagaagaagacaaaca 159  
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 Db 191 TGTGGCCTCAGCTGAGGTGCTGCTGTGGAAGAACCTCAGTTTCAGAGAAGACAAACA 250

RESULT 22  
 LOCUS AX139817 9741 bp DNA linear PAT 30-MAY-2001  
 DEFINITION Sequence 69 from Patent EP1096012.  
 ACCESSION AX139817  
 VERSION AX139817.1 GI:14275399  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 9741)  
 Deneffe, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,  
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,  
 Remaley, A., Brewer, H.B. and Dean, M.  
 Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: EP 1096012-A 69 02-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
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BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others  
 ORIGIN

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BASE COUNT      2650 a 2180 c 2290 g 2620 t 1 others
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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 23
AX127831
LOCUS          AX127831
DEFINITION    Sequence 70 from Patent WO0130848.
ACCESSION     AX127831
VERSION       AX127831.1 GI:14134478
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE        Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P.,
AUTHORS      Brewer, B., Duverger, N., Remaley, A., and Santamarina-Fojo, S.
TITLE        Regulatory nucleic acid sequences of the abcl gene
JOURNAL       Patent: WO 0130848-A 10 08-NOV-2001;
              Aventis Pharma S.A. (FR)
FEATURES
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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS          AX127831
DEFINITION    Sequence 70 from Patent WO0130848.
ACCESSION     AX127831
VERSION       AX127831.1 GI:14134478
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE        Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P.,
AUTHORS      Brewer, B., Duverger, N., Remaley, A., and Santamarina-Fojo, S.
TITLE        Regulatory nucleic acid sequences of the abcl gene
JOURNAL       Patent: WO 0130848-A 10 03-MAY-2001;
              Aventis Pharma S.A. (FR)
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RESULT 25
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LOCUS          AX139818
DEFINITION    Sequence 70 from Patent EP1096012.
ACCESSION     AX139818
VERSION       AX139818.1 GI:14275400
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE        Deneffe, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
AUTHORS      Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
TITLE        Remaley, A., Brewer, H.B. and Dean, M.
TITLE        Nucleic acids of the human abcl gene and their therapeutic and
JOURNAL       diagnostic application
JOURNAL       Patent: EP 1096012-A 70 02-MAY-2001;
              Aventis Pharma S.A. (FR)
FEATURES
source       Location/Qualifiers
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ORIGIN

Query Match
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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 ttgtggcctcagctgaggttgcgtgtggaagaacctcactttcagaagaagacaaca 159
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Db 304 TGTGGCCTCAGCTGAGGTGCTGCTGTGGAGAACCTCCTTTTCAGAGAAGACAACA 363

RESULT 26
AL353685/c
LOCUS          AL353685/c
DEFINITION    Human DNA sequence from clone RP11-31J20 on chromosome 9, complete
ACCESSION     AL353685
VERSION       AL353685.23 GI:14329534
KEYWORDS      HTG.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE        Tracey, A.
AUTHORS      Direct Submission
JOURNAL       Submitted (01-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
              CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
              requests: clonerequest@sanger.ac.uk
              On Jun 8, 2001 this sequence version replaced gi:14272260.
              During sequence assembly data is compared from overlapping clones.
              Where differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the
              variation annotation may not be found in the sequence submission
              corresponding to the overlapping clone, as we submit sequences with
              only a small overlap as described above.
              This sequence was finished as follows unless otherwise noted: all

```

regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the abbreviations are confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; SW.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/projects/C-elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9> RP11-31J20 is from the library RPCR-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-31J20. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-31J20 is at 129608 in this sequence. The true right end of clone RP11-413C10 is at 2000 in this sequence.

## FEATURES

## Location/Qualifiers

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 /chromosome="9"  
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 repeat\_region 2496..2714  
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 repeat\_region 2777..2896  
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 repeat\_region 3237..3415  
 /note="L1ME repeat: matches 5696. .5821 of consensus"  
 repeat\_region 6522..6818  
 /note="AluSq repeat: matches 1. .295 of consensus"  
 repeat\_region 7282..7415  
 /note="L1WB8 repeat: matches 6040. .6173 of consensus"  
 repeat\_region 8145..8434  
 /note="AluSc repeat: matches 1. .298 of consensus"  
 repeat\_region 12145..12713  
 /note="L2 repeat: matches 1363. .1940 of consensus"  
 repeat\_region 13890..13969  
 /note="L2 repeat: matches 2611. .2701 of consensus"  
 repeat\_region 15380..15411  
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 repeat\_region 16105..16144  
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 repeat\_region 16868..17049  
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 repeat\_region 17941..18229  
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 repeat\_region 18259..18553  
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 repeat\_region 20310..20616  
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 repeat\_region 20957..21107  
 /note="MIR repeat: matches 49. .212 of consensus"  
 repeat\_region 21783..22078  
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 repeat\_region 22320..22439  
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 repeat\_region 22533..22839  
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 repeat\_region 23427..23945

repeat\_region 24245..24544  
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 repeat\_region 24536..24587  
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 repeat\_region 26504..26561  
 /note="29 copies 2 mer ta 69% conserved"  
 repeat\_region 26849..26892  
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 repeat\_region 28515..28626  
 /note="MIR repeat: matches 17. .129 of consensus"  
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 repeat\_region 31424..31734  
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 repeat\_region 31987..32116  
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 repeat\_region 34729..34873  
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 repeat\_region 39674..40243  
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 repeat\_region 50189..50347  
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 repeat\_region 54754..55032  
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 repeat\_region 55042..55343  
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\* 52719 56592: contig of 3874 bp in length  
\* 56593 56692: gap of 100 bp  
\* 56693 59635: contig of 2943 bp in length  
\* 59636 59735: gap of 100 bp  
\* 59736 63661: contig of 3926 bp in length  
\* 63662 63761: gap of 100 bp  
\* 63762 68437: contig of 4676 bp in length  
\* 68438 68537: gap of 100 bp  
\* 68538 71458: contig of 2921 bp in length  
\* 71459 71558: gap of 100 bp  
\* 71559 76888: contig of 5330 bp in length  
\* 76889 76988: gap of 100 bp  
\* 76989 82113: contig of 5125 bp in length  
\* 82114 82213: gap of 100 bp  
\* 82214 88220: contig of 6007 bp in length  
\* 88221 88320: gap of 100 bp  
\* 88321 93499: contig of 5179 bp in length  
\* 93500 93599: gap of 100 bp  
\* 93600 97901: contig of 4302 bp in length  
\* 97902 98001: gap of 100 bp  
\* 98002 103016: contig of 5015 bp in length  
\* 103017 103116: gap of 100 bp  
\* 103117 109178: contig of 6062 bp in length  
\* 109179 109278: gap of 100 bp  
\* 109279 117307: contig of 8029 bp in length  
\* 117308 117407: gap of 100 bp  
\* 117408 124079: contig of 6672 bp in length  
\* 124080 124179: gap of 100 bp  
\* 124180 131281: contig of 7102 bp in length  
\* 131282 131381: gap of 100 bp  
\* 131382 138059: contig of 6678 bp in length  
\* 138060 138159: gap of 100 bp  
\* 138160 143491: contig of 7332 bp in length  
\* 143492 145591: gap of 100 bp  
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\* 157392 157491: gap of 100 bp  
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## FEATURES

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Best Local Similarity 100.0%; Pred. No. 7.9e-23;

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AX092589

LOCUS

AX092589 Sequence 1 from Patent WO0115676. DNA linear PAT 21-MAR-2001

ACCESSION AX092589

VERSION AX092589.1 GI:13444647

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

REFERENCE

1 (bases 1 to 183999)

AUTHORS

Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.

Compositions and methods for modulating hdl cholesterol and

TITLE

triglyceride levels

JOURNAL

Patent: WO 0115676-A 1 08-MAR-2001;

FEATURES

University of British Columbia (CA) ; Xenon Genetics Inc. (CA)

Location/Qualifiers

1..183999

/organism="Homo sapiens"

BASE COUNT

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ORIGIN

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RESULT 29

AF287262

LOCUS

AF287262 Homo sapiens Atp-binding cassette 1 sub-family A member 1 (ABCA1)

DEFINITION

and SNAP protein genes, complete cds.

ACCESSION

AF287262

AF287262.1 GI:13876612  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 201144)  
 Qiu, Y., Cavellier, L., Chiu, S., Yang, X., Rubin, E. and Cheng, J.-F.  
 Human and mouse abcal comparative sequencing and transgenesis  
 studies revealing novel regulatory sequences  
 Genomics 73 (1), 66-76 (2001)  
 JOURNAL 21251004  
 MEDLINE 2 (bases 1 to 201144)  
 Qiu, Y., Cavellier, L., Chiu, S., Rubin, E. and Cheng, J.-F.  
 Direct Submision  
 TITLE Submitted (13-JUL-2000) Genome Science Department, Lawrence  
 JOURNAL Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,  
 CA 94720, USA  
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Qy 100 tgtgtgctcagctgaggtgtgtgtgtggaagaaacctcactttcagaagaagacaaca 159  
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RESULT 30

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LOCUS Homo sapiens cDNA FLJ14266 fis, clone PLACE1002437, highly similar
to ATP-BINDING CASSETTE TRANSPORTER 1.
DEFINITION AK024328
ACCESSION AK024328.1 GI:10436685
VERSION oligo capping; fis (full insert sequence).
KEYWORDS Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

# REFERENCE

## AUTHORS

# 1 (sites)

Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.  
 NEDO human cDNA sequencing project  
 Unpublished (2000)

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3951, Fax: 81-438-52-3952)  
 NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

## FEATURES

## source

## Location/Qualifiers

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 329 CAGCTGAGGTGTGTGTGTGGAAGAACCTCCTTTCAGAAGAGACAACA 379

## RESULT 31

## AC021345/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

AC021345 90698 bp DNA linear HTG 13-JUL-2000  
 Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.  
 AC021345  
 AC021345.2 GI:9130845  
 HTG; PHASE0.  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90698)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-24J9

Unpublished

2 (bases 1 to 90698)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,

Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
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Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,  
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MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,  
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Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,  
Zimmer, A. and Zody, M.

# TITLE JOURNAL

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6705761.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L4483

Center clone name: 24\_J\_9

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\* NOTE: This record contains 92 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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911 1010: gap of 100 bp  
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ACCESSION AX092705  
VERSION AX092705.1 GI:13444762  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.  
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels  
JOURNAL Patent: WO 0115676-A 117 08-MAR-2001;  
University of British Columbia (CA); Xenon Genetics Inc. (CA)  
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 accagccagggcgctccctgc 27  
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Db 1 ACCAGCCAGGGCGCTCCCTGC 21

RESULT 34  
AX092707 21 bp DNA linear PAT 21-MAR-2001  
LOCUS Sequence 119 from Patent WO0115676.  
DEFINITION AX092707  
ACCESSION AX092707  
VERSION AX092707.1 GI:13444764  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.  
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels  
JOURNAL Patent: WO 0115676-A 119 08-MAR-2001;  
University of British Columbia (CA); Xenon Genetics Inc. (CA)  
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LOCUS Sequence 255 from Patent WO0115676.  
DEFINITION AX092843  
ACCESSION AX092843  
VERSION AX092843.1 GI:13444900  
KEYWORDS synthetic construct.  
SOURCE synthetic construct  
ORGANISM artificial sequence.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.  
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels  
JOURNAL Patent: WO 0115676-A 255 08-MAR-2001;  
University of British Columbia (CA); Xenon Genetics Inc. (CA)  
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LOCUS Homo sapiens clone NM0395B14, complete sequence.
DEFINITION AC007388
ACCESSION AC007388
VERSION AC007388.3 GI:5931452
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Waterston, R.H.
TITLE The sequence of Homo sapiens clone
REFERENCE 2 (bases 1 to 151961)
AUTHORS Waterston, R.H.
JOURNAL Direct Submission
TITLE Submitted (25-APR-1999) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 151961)
AUTHORS Waterston, R.H.
JOURNAL Direct Submission
TITLE Submitted (28-SEP-1999) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Sep 28, 1999 this sequence version replaced gi:5103896.
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1..151961
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NM0395B14"
BASE COUNT 47610 a 31316 c 31453 g 41582 t
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Query Match 12.6%; Score 20; DB 9; Length 151961;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 cactttcagaagaagacaaa 157
|||||
Db 9177 CACTTTCAGAGAGACAAA 9158

RESULT 36
AR066487
LOCUS AR066487 624 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5850020.
ACCESSION AR066487
VERSION AR066487.1 GI:5996703
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 624)
AUTHORS Blosberg, L.N., Havukkala, I., and Grierson, A.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 5850020-A 9 15-DEC-1998;
FEATURES
source
Location/Qualifiers
1..624
/organism="unknown"
BASE COUNT 136 a 188 c 188 g 111 t 1 others
ORIGIN

Query Match 11.9%; Score 19; DB 6; Length 624;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctggcgctgctgctgag 88
|||||
Db 261 GCTGGCGCTGCTGCTGAG 279

RESULT 37
AR074100
LOCUS AR074100 624 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 9 from patent US 5952486.
ACCESSION AR074100
VERSION AR074100.1 GI:10000860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 624)
AUTHORS Blosberg, L.N., Havukkala, I., and Grierson, A.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 5952486-A 9 14-SEP-1999;
FEATURES
source
Location/Qualifiers
1..624
/organism="unknown"
BASE COUNT 136 a 188 c 188 g 111 t 1 others
ORIGIN

Query Match 11.9%; Score 19; DB 6; Length 624;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctggcgctgctgctgag 88
|||||
Db 261 GCTGGCGCTGCTGCTGAG 279

RESULT 38
AR143612
LOCUS AR143612 624 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6204434.
ACCESSION AR143612
VERSION AR143612.1 GI:15104898
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 624)
AUTHORS Blosberg, L.N., Havukkala, I., and Grierson, A.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 6204434-A 9 20-MAR-2001;
FEATURES
source
Location/Qualifiers
1..624
/organism="unknown"
BASE COUNT 136 a 188 c 188 g 111 t 1 others
ORIGIN

Query Match 11.9%; Score 19; DB 6; Length 624;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 261 GCTGGCGCTGCTGCTGAG 279

RESULT 39
BD005648
LOCUS BD005648 624 bp DNA linear PAT 31-JAN-2002
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD005648
VERSION BD005648.1 GI:18634019
KEYWORDS JP 2001500378-A/9.

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SOURCE      unidentified.
ORGANISM     unidentified.
REFERENCE    1 (bases 1 to 624)
AUTHORS      Bloksberg,L.N., Grierson,A.W. and Havukkala,I.J.
TITLE        Materials and methods for the modification of plant lignin content
JOURNAL      Patent: JP 2001500378-A 9 16-JAN-2001;
              GENESIS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS
LTD
COMMENT      OS      Unidentified
              PN      JP 2001500378-A/9
              PD      16-JAN-2001
              PF      10-SEP-1997 JP 1998513535
              PR      11-SEP-1996 US 08/713000
              PI      LEONARD NATHAN BLOKSBERG,ALISTAIR WALLACE GRIERSON, PI ILKKA
              JAAKKO HAVUKKALA
              PC      C12N15/53,C12N15/54,C12N15/52,C12N15/60,C12N15/82,A01H5/00 CC
              Strandedness: Single;
              CC      Topology: Linear;
              FH      Key      Location/Qualifiers
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                               /db_xref='taxon:32644'
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 gctggcgctgctgctgag 88
|||||
Db 261 GCTGGCGTCTGGCTGAG 279

RESULT 40
AR074136      684 bp      DNA      linear      PAT 28-AUG-2000
LOCUS
DEFINITION    Sequence 45 from patent US 5952486.
ACCESSION     AR074136
VERSION       AR074136.1 GI:10000896
KEYWORDS      Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 684)
AUTHORS      Bloksberg,L.N., Havukkala,I. and Grierson,A.W.
TITLE        Materials and methods for the modification of plant lignin content
JOURNAL      Patent: US 5952486-A 45 14-SEP-1999;
              Location/Qualifiers
FEATURES      source      1..684
                               /organism='unknown'
BASE COUNT    150 a 207 c 200 g 127 t
ORIGIN
Query Match  11.9%; Score 19; DB 6; Length 684;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 gctggcgctgctgctgag 88
|||||
Db 261 GCTGGCGTCTGGCTGAG 279

SOURCE      unidentified.
ORGANISM     unidentified.
REFERENCE    1 (bases 1 to 624)
AUTHORS      Bloksberg,L.N., Grierson,A.W. and Havukkala,I.J.
TITLE        Materials and methods for the modification of plant lignin content
JOURNAL      Patent: JP 2001500378-A 9 16-JAN-2001;
              GENESIS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS
LTD
COMMENT      OS      Unidentified
              PN      JP 2001500378-A/45
              PD      16-JAN-2001
              PF      10-SEP-1997 JP 1998513535
              PR      11-SEP-1996 US 08/713000
              PI      LEONARD NATHAN BLOKSBERG,ALISTAIR WALLACE GRIERSON, PI ILKKA
              JAAKKO HAVUKKALA
              PC      C12N15/53,C12N15/54,C12N15/52,C12N15/60,C12N15/82,A01H5/00 CC
              Strandedness: Single;
              CC      Topology: Linear;
              FH      Key      Location/Qualifiers
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                               /db_xref='taxon:32644'
BASE COUNT    150 a 207 c 200 g 127 t
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Query Match  11.9%; Score 19; DB 6; Length 684;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 gctggcgctgctgctgag 88
|||||
Db 261 GCTGGCGTCTGGCTGAG 279

RESULT 42
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LOCUS
DEFINITION    Homo sapiens mRNA for KIAA0624 protein, partial cds.
ACCESSION     AB014524
VERSION       AB014524.1 GI:3327061
KEYWORDS      Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII
              SK plus clone:HG04767.
ORGANISM      Homo sapiens
REFERENCE     1 (bases 1 to 6542)
AUTHORS      Ohara,O., Suyama,M., Nagase,T. and Ishikawa,K.
TITLE        Direct Submission
JOURNAL      Submitted (26-MAY-1998) Osamu Ohara, Kazusa DNA Research Institute,
              Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
              292-0812, Japan (E-mail:cdna1nfo@kazusa.or.jp, Tel:+81-438-52-3913,
              Fax:+81-438-52-3914)
              2 (sites)
              Ishikawa,K., Nagase,T., Suyama,M., Miyajima,N., Tanaka,A.,
              Kotani,H., Nomura,N. and Ohara,O.
              Prediction of the coding sequences of unidentified human genes. X.
              The complete sequences of 100 new cDNA clones from brain which can
              code for large proteins in vitro
              DNA Res. 5 (3), 169-176 (1998)
              98403880
              Location/Qualifiers
              1..6542
              /organism='Homo sapiens'
              /db_xref='taxon:9606'

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Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jul 13, 2000 this sequence version replaced gi:6403649.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L3053  
 Center clone name: 10\_E\_16  
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\* NOTE: This record contains 72 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

1 820: contig of 820 bp in length  
 821 920: gap of 100 bp  
 921 1730: contig of 810 bp in length  
 1731 1830: gap of 100 bp  
 1831 2644: contig of 814 bp in length  
 2645 2744: gap of 100 bp  
 2745 3547: contig of 803 bp in length  
 3548 3647: gap of 100 bp  
 3648 4437: contig of 790 bp in length  
 4438 4537: gap of 100 bp  
 4538 5340: contig of 803 bp in length  
 5341 5440: gap of 100 bp  
 5441 6217: contig of 777 bp in length  
 6218 6317: gap of 100 bp  
 6318 7106: contig of 789 bp in length  
 7107 7206: gap of 100 bp  
 7207 8003: contig of 797 bp in length  
 8004 8103: gap of 100 bp  
 8104 8893: contig of 790 bp in length  
 8894 8993: gap of 100 bp  
 8994 9706: contig of 713 bp in length  
 9707 9806: gap of 100 bp  
 9807 10597: contig of 791 bp in length  
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 11498 11597: gap of 100 bp  
 11598 12413: contig of 816 bp in length  
 12414 12513: gap of 100 bp  
 12514 13325: contig of 812 bp in length  
 13326 13425: gap of 100 bp  
 13426 14213: contig of 788 bp in length  
 14214 14313: gap of 100 bp  
 14314 15081: contig of 768 bp in length  
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 17941 18743: contig of 803 bp in length  
 18744 18843: gap of 100 bp  
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 19548 19647: gap of 100 bp  
 19648 20462: contig of 815 bp in length

20463 20562: gap of 100 bp  
 20563 21327: contig of 765 bp in length  
 21328 21477: gap of 100 bp  
 21478 22219: contig of 792 bp in length  
 22220 22319: gap of 100 bp  
 22320 23125: contig of 806 bp in length  
 23126 23225: gap of 100 bp  
 23226 24025: contig of 800 bp in length  
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 38402 39181: contig of 780 bp in length  
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 51712 52514: contig of 803 bp in length  
 52515 52614: gap of 100 bp

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 \* 53526 54329: contig of 804 bp in length  
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 \* 55248 55347: gap of 100 bp  
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 \* 56150 56249: gap of 100 bp  
 \* 56250 56953: contig of 704 bp in length  
 \* 56954 57053: gap of 100 bp  
 \* 57054 57865: contig of 812 bp in length  
 \* 57866 57965: gap of 100 bp  
 \* 57966 58759: contig of 794 bp in length  
 \* 58760 58859: gap of 100 bp  
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 \* 59637 59736: gap of 100 bp  
 \* 59737 60441: contig of 705 bp in length  
 \* 60442 60541: gap of 100 bp  
 \* 60542 61327: contig of 786 bp in length  
 \* 61328 61427: gap of 100 bp  
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 \* 62218 62317: gap of 100 bp  
 \* 62318 63129: contig of 812 bp in length  
 \* 63130 63229: gap of 100 bp  
 \* 63230 64041: contig of 812 bp in length.

FEATURES  
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Query Match 11.9%; Score 19; DB 2; Length 64041;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 cccgtgctgcagctctggc 40  
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 Db 22122 CCTGCTGTCAGCTCTGGC 22104

RESULT 45  
 AL591133  
 LOCUS Human DNA sequence from clone RP11-12116 on chromosome 9, complete  
 DEFINITION  
 sequence.  
 ACCESSION AL591133  
 VERSION AL591133.7 GI:15982094  
 KEYWORDS HTG.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 66477)  
 Sehra, H.  
 Direct Submission  
 Submitted (04-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk  
 On Oct 5, 2001 this sequence version replaced gi:14787626.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.

COMMENT  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em: EMBL; Sw:  
 SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP  
 database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
 Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr9  
 RP11-12116 is from the library RPCI-11.1 constructed by the group  
 of Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone  
 RP11-12116 it may be shorter because we sequence overlapping  
 sections only once, except for a short overlap.  
 The true left end of clone RP11-14116 is at 64478 in this  
 sequence. The true right end of clone RP11-338L20 is at 2000 in  
 this sequence.

FEATURES  
 Location/Qualifiers  
 source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
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 ORIGIN

Query Match 11.9%; Score 19; DB 9; Length 66477;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 tttcagaagaagacaaaca 159  
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 Db 19651 TTTCAGAAAGAACAAACA 19669

Search completed: September 20, 2002, 06:33:24  
 Job time: 18598 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 06:08:05 ; Search time 521.76 Seconds  
(without alignments)  
523.209 Million cell updates/sec

Title: US-09-846-456-5  
Perfect score: 159  
Sequence: 1 ttaatgaccagccacggcg.....ctttcagaagaagacaaca 159

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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24: /SIDSL1/gcgdata/hold-geneseg/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	77	48.4	10442	22 AAF24680 Nucleotide sequenc
2	77	48.4	10442	22 AAF24702 Nucleotide sequenc
3	77	48.4	10474	22 AAF24685 Nucleotide sequenc
4	77	48.4	10474	22 AAF24686 Nucleotide sequenc
5	77	48.4	10474	22 AAF24707 Nucleotide sequenc
6	77	48.4	10474	22 AAF24708 Nucleotide sequenc
7	60	37.7	446	22 AAS04035 Partial human ABC1
8	60	37.7	7086	22 ABA09200 Human ABC1 homolo
9	60	37.7	7086	22 AAK52667 Human polynucleoti

10	60	37.7	7260	22 AAD21326 Human ATP binding
11	60	37.7	7260	22 AAI70315 Human ATP binding
12	60	37.7	7281	22 AAK51683 Human polynucleoti
13	60	37.7	7857	21 AAC69388 Human ABC1 choles
14	60	37.7	7860	22 AAF83826 Human ABC1 choles
15	60	37.7	7860	22 AAF92835 Human ABC1 cdNA.
16	60	37.7	7861	21 AAC69387 Human ABC1 choles
17	60	37.7	7864	21 AAC69120 Human ABC1 choles
18	60	37.7	7864	21 AAC69385 Human ABC1 choles
19	60	37.7	7864	21 AAC69386 Human ABC1 choles
20	60	37.7	7864	21 AAC69389 Human ABC1 choles
21	60	37.7	9741	22 AAS06120 Human ABC1 DNA seq
22	60	37.7	9854	22 AAC69132 Human ABC1 gene ex
23	60	37.7	10545	21 AAC69121 Human ABC1 genomic
24	60	37.7	183999	22 AAF92831 Human cdNA clone (
25	51	32.1	736	22 AAH07432 ABC1 polymorphism
26	51	32.1	1556	22 AAH18606 Human ABC1 gene pr
27	35	22.0	37	22 AAF93084 Human ABC1 gene pr
28	21	13.2	21	21 AAC69306 Polymorphic sequen
29	21	13.2	21	21 AAC69308 Polymorphic sequen
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31	21	13.2	21	22 AAF92948 Plant PAL enzyme D
32	19	11.9	577	21 AAA68004 pine phenylalanine
33	19	11.9	624	19 AAU23916 pinus radiata PAL
34	19	11.9	624	20 AAU206895 plant PAL enzyme D
35	19	11.9	624	21 AAF67916 pine phenylalanine
36	19	11.9	684	19 AAU23865 pinus radiata phen
37	19	11.9	684	20 AAU206898 pinus radiata PAL
38	19	11.9	684	21 AAF67952 DNA encoding novel
39	19	11.9	684	21 AAF67952 DNA encoding novel
40	19	11.9	5286	23 AAS73156 DNA encoding novel
41	19	11.9	5954	23 AAS80591 DNA encoding novel
42	19	11.9	6143	23 AAS83843 Human ABC1 phospho
43	18	11.3	18	21 AAC69153 Drosophila melanog
44	18	11.3	6420	23 ABL08833 Drosophila melanog
45	18	11.3	11580	23 ABL08832 Drosophila melanog

## ALIGNMENTS

### RESULT 1

AAF24680  
ID AAF24680 standard; DNA: 10442 BP.

XX AAF24680;

AC AAF24680;

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of a human ABC1 polypeptide.

Human; adenosine triphosphate binding cassette protein 1; ABC1;  
apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
atherosclerosis; cholesterol transport; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 291..7076

XX FT /\*tag= a

XX FT /product= "ABC1 polypeptide"

XX WO200078972-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16765.

XX 18-JUN-1999; 99US-0140264.

XX 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

PA (CVTH-) CV THERAPEUTICS INC.  
 XX Lawn RM, Wade D, Garvin M;  
 XX WPI; 2001-137812/14.  
 DR Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 XX useful for the development of agents for the treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX  
 PS Disclosure; Page 122-128; 215pp; English.  
 XX  
 CC The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
 CC membranes and utilises ATP hydrolysis to transport a wide variety of  
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in  
 CC the apolipoprotein-mediated mobilisation of intracellular cholesterol  
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder  
 CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
 CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are  
 CC useful for developing pharmaceutical agents for the treatment of heart  
 CC disease and other disorders associated with hypercholesterolemia and  
 CC atherosclerosis. The genes are useful for developing screening assays to  
 CC screen for compounds that regulate the expression of genes associated  
 CC with cholesterol transport. The genes and proteins are also useful for  
 CC are also useful as diagnostic indicators of cardiovascular disease and  
 CC other disorders associated with hypercholesterolemia.  
 XX  
 SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 48.4%; Score 77; DB 22; Length 10442;  
 Best Local Similarity 99.2%; Pred. No. 5e-29;  
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 agctctggccgtcctccagggtcccgagccacacgtggcgctggtgagga 91  
 Db |||||||  
 QY 229 agctctggccgtcctccagggtcccgagccacacgtggcgctggtgagga 288  
 Db |||||||

QY 92 acatggcatgttgccctcagctgaggtgctgtggaagaacctcactttcagaagaa 151  
 Db |||||||  
 QY 289 acatggctgttgccctcagctgaggtgctgtggaagaacctcactttcagaagaa 348  
 Db |||||||

QY 152 gacaaaca 159  
 Db |||||||

QY 349 gacaaaca 356  
 Db |||||||

RESULT 2  
 AAF24702  
 ID AAF24702 standard; DNA; 10442 BP.  
 XX  
 AC AAF24702;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a human ABC1 polypeptide.  
 XX  
 KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 291..7076  
 FT /\*tag= a  
 FT /product= "ABC1 polypeptide"  
 FT  
 PN WO200078971-A2.  
 XX

PD 28-DEC-2000.  
 XX 16-JUN-2000; 2000WO-US16591.  
 XX 18-JUN-1999; 99US-0140264.  
 PR 14-SEP-1999; 99US-0153872.  
 PR 19-NOV-1999; 99US-0166573.  
 XX (CVTH-) CV THERAPEUTICS INC.  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Lawn RM, Wade D, Oram JF, Garvin M;  
 XX WPI; 2001-137811/14.  
 DR P-PSDB; AAB31365.  
 XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
 PT polynucleotides and polypeptides, useful for treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX  
 PS Claim 3; Page 117-123; 211pp; English.  
 XX  
 CC The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
 CC membranes and utilises ATP hydrolysis to transport a wide variety of  
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in  
 CC the apolipoprotein-mediated mobilisation of intracellular cholesterol  
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder  
 CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
 CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are  
 CC useful for developing pharmaceutical agents for the treatment of heart  
 CC disease and other disorders associated with hypercholesterolemia and  
 CC atherosclerosis. The genes are useful for developing screening assays to  
 CC screen for compounds that regulate the expression of genes associated  
 CC with cholesterol transport. The genes and proteins are also useful for  
 CC are also useful as diagnostic indicators of cardiovascular disease and  
 CC other disorders associated with hypercholesterolemia.  
 XX  
 SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 48.4%; Score 77; DB 22; Length 10442;  
 Best Local Similarity 99.2%; Pred. No. 5e-29;  
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 agctctggccgtcctccagggtcccgagccacacgtggcgctggtgagga 91  
 Db |||||||  
 QY 229 agctctggccgtcctccagggtcccgagccacacgtggcgctggtgagga 288  
 Db |||||||

QY 92 acatggcatgttgccctcagctgaggtgctgtggaagaacctcactttcagaagaa 151  
 Db |||||||  
 QY 289 acatggctgttgccctcagctgaggtgctgtggaagaacctcactttcagaagaa 348  
 Db |||||||

QY 152 gacaaaca 159  
 Db |||||||

QY 349 gacaaaca 356  
 Db |||||||

RESULT 3  
 AAF24685  
 ID AAF24685 standard; DNA; 10474 BP.  
 XX  
 AC AAF24685;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
 XX  
 KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.

XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX DE CDS 323..7108  
 FT FT /\*tag= a  
 FT FT /product= "defective ABC1 polypeptide"  
 XX PN WO200078972-A2.  
 XX PD 28-DEC-2000.  
 XX XX 16-JUN-2000; 2000WO-US16765.  
 XX PF 18-JUN-1999; 99US-0140264.  
 XX PR 14-SEP-1999; 99US-0153872.  
 XX PR 19-NOV-1999; 99US-0166573.  
 XX XX (CVTH-) CV THERAPEUTICS INC.  
 XX PA Lawn RM, Wade D, Garvin M;  
 XX PI WPI; 2001-137812/14.  
 XX DR Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 XX PT useful for the development of agents for the treatment of heart disease  
 XX PT and other disorders associated with hypercholesterolemia and  
 XX PT atherosclerosis -  
 XX PS Disclosure; Page 148-154; 215pp; English.  
 XX XX The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
 CC ATP hydrolysis to transport a wide variety of substrates across the  
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
 CC Tangier disease, a genetic disorder characterised by abnormal  
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
 CC pharmaceutical agents for the treatment of heart disease and other  
 CC disorders associated with hypercholesterolemia and atherosclerosis. The  
 CC genes are useful for developing screening assays to screen for compounds  
 CC that regulate the expression of genes associated with cholesterol  
 CC transport. The genes and proteins are also useful for are also useful  
 CC as diagnostic indicators of cardiovascular disease and other disorders  
 CC associated with hypercholesterolemia.  
 XX XX Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;  
 XX SQ  
 Query Match 48.4%; Score 77; DB 22; Length 10474;  
 Best Local Similarity 99.2%; Pred. No. 5e-29;  
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 32 agctctggcgcgtgcttccagggtcccgagccacacgtggcgctgctgaagga 91  
 Db 261 agctctggcgcgtgcttccagggtcccgagccacacgtggcgctgctgaagga 320  
 QY 92 acatggcatgttgctcagctgaggtgctgtgtggaagaacctcactttcagaagaa 151  
 Db 321 acatgctgtgtgctcagctgaggtgctgtgtggaagaacctcactttcagaagaa 380  
 QY 152 gacaaaca 159  
 Db 381 gacaaaca 388  
 RESULT 4  
 AAF24686  
 ID AAF24686 standard; DNA; 10474 BP.  
 XX  
 AC AAF24686;

XX DT 20-APR-2001 (first entry)  
 XX DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
 XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 XX OS Homo sapiens.  
 XX XX Location/Qualifiers  
 XX FH Key 323..7108  
 XX DE CDS /\*tag= a  
 XX FT FT /product= "defective ABC1 polypeptide"  
 XX XX WO200078972-A2.  
 XX PD 28-DEC-2000.  
 XX XX 16-JUN-2000; 2000WO-US16765.  
 XX PF 18-JUN-1999; 99US-0140264.  
 XX PR 14-SEP-1999; 99US-0153872.  
 XX PR 19-NOV-1999; 99US-0166573.  
 XX XX (CVTH-) CV THERAPEUTICS INC.  
 XX PA Lawn RM, Wade D, Garvin M;  
 XX PI WPI; 2001-137812/14.  
 XX DR Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 XX PT useful for the development of agents for the treatment of heart disease  
 XX PT and other disorders associated with hypercholesterolemia and  
 XX PT atherosclerosis -  
 XX PS Disclosure; Page 170-176; 215pp; English.  
 XX XX The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
 CC ATP hydrolysis to transport a wide variety of substrates across the  
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
 CC Tangier disease, a genetic disorder characterised by abnormal  
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
 CC pharmaceutical agents for the treatment of heart disease and other  
 CC disorders associated with hypercholesterolemia and atherosclerosis. The  
 CC genes are useful for developing screening assays to screen for compounds  
 CC that regulate the expression of genes associated with cholesterol  
 CC transport. The genes and proteins are also useful for are also useful  
 CC as diagnostic indicators of cardiovascular disease and other disorders  
 CC associated with hypercholesterolemia.  
 XX XX Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;  
 XX SQ  
 Query Match 48.4%; Score 77; DB 22; Length 10474;  
 Best Local Similarity 99.2%; Pred. No. 5e-29;  
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 32 agctctggcgcgtgcttccagggtcccgagccacacgtggcgctgctgaagga 91  
 Db 261 agctctggcgcgtgcttccagggtcccgagccacacgtggcgctgctgaagga 320  
 QY 92 acatggcatgttgctcagctgaggtgctgtgtggaagaacctcactttcagaagaa 151  
 Db 321 acatgctgtgtgctcagctgaggtgctgtgtggaagaacctcactttcagaagaa 380  
 QY 152 gacaaaca 159

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Db      381 gacaaaca 388
      |||||
RESULT      5
AAF24707
ID      AAF24707 standard; DNA; 10474 BP.
XX
AC      AAF24707;
XX
DT      20-APR-2001 (first entry)
XX
DE      Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW      Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW      apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW      chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW      atherosclerosis; cholesterol transport; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      323..7108
          /*tag= a
          /product= "defective ABC1 polypeptide"
XX
PN      WO200078971-A2.
XX
PD      28-DEC-2000.
XX
PF      16-JUN-2000; 2000WO-US16591.
XX
PR      18-JUN-1999; 99US-0140264.
PR      14-SEP-1999; 99US-0153872.
PR      19-NOV-1999; 99US-0166573.
XX
PA      (CVTH-) CV THERAPEUTICS INC.
PA      (UNIW ) UNIV WASHINGTON.
XX
PI      Lawn RM, Wade D, Oram JF, Garvin M;
XX
WPI; 2001-137811/14.
DR      P-PSDB; AAB31366.
XX
PT      Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT      polynucleotides and polypeptides, useful for treatment of heart disease
PT      and other disorders associated with hypercholesterolemia and
PT      atherosclerosis -
XX
PS      Claim 27; Page 144-150; 211pp; English.
XX
CC      The present sequence encodes a human adenosine triphosphate (ATP)
CC      binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC      a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC      ATP hydrolysis to transport a wide variety of substrates across the
CC      plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC      mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC      Tangier disease, a genetic disorder characterised by abnormal
CC      HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC      9q22-9q31. The ABC1 genes and proteins are useful for developing
CC      pharmaceutical agents for the treatment of heart disease and other
CC      disorders associated with hypercholesterolemia and atherosclerosis. The
CC      genes are useful for developing screening assays to screen for compounds
CC      that regulate the expression of genes associated with cholesterol
CC      transport. The genes and proteins are also useful for are also useful
CC      as diagnostic indicators of cardiovascular disease and other disorders
CC      associated with hypercholesterolemia.
XX
SQ      Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

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Query Match      48.4%; Score 77; DB 22; Length 10474;
Best Local Similarity 99.2%; Pred. No. 5e-29;

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Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      32 agctctggcgcgtgctccagggctccagccacacgctggcgtgctgggga 91
      |||||
Db      261 agctctggcgcgtgctccagggctccagccacacgctggcgtgctgggga 320
      |||||
QY      92 acatggcatgttgccctcagctgaggttgctgctgtggaagaacctcactttcagaaga 151
      |||||
Db      321 acatggctgttgccctcagctgaggttgctgctgtggaagaacctcactttcagaaga 380
      |||||
QY      152 gacaaaca 159
      |||||
Db      381 gacaaaca 388

RESULT      6
AAF24708
ID      AAF24708 standard; DNA; 10474 BP.
XX
AC      AAF24708;
XX
DT      20-APR-2001 (first entry)
XX
DE      Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW      Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW      apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW      chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW      atherosclerosis; cholesterol transport; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      323..7108
          /*tag= a
          /product= "defective ABC1 polypeptide"
XX
PN      WO200078971-A2.
XX
PD      28-DEC-2000.
XX
PF      16-JUN-2000; 2000WO-US16591.
XX
PR      18-JUN-1999; 99US-0140264.
PR      14-SEP-1999; 99US-0153872.
PR      19-NOV-1999; 99US-0166573.
XX
PA      (CVTH-) CV THERAPEUTICS INC.
PA      (UNIW ) UNIV WASHINGTON.
XX
PI      Lawn RM, Wade D, Oram JF, Garvin M;
XX
WPI; 2001-137811/14.
DR      P-PSDB; AAB31367.
XX
PT      Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT      polynucleotides and polypeptides, useful for treatment of heart disease
PT      and other disorders associated with hypercholesterolemia and
PT      atherosclerosis -
XX
PS      Claim 30; Page 165-172; 211pp; English.
XX
CC      The present sequence encodes a human adenosine triphosphate (ATP)
CC      binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC      a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC      ATP hydrolysis to transport a wide variety of substrates across the
CC      plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC      mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC      Tangier disease, a genetic disorder characterised by abnormal
CC      HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC      9q22-9q31. The ABC1 genes and proteins are useful for developing
CC      pharmaceutical agents for the treatment of heart disease and other
CC      disorders associated with hypercholesterolemia and atherosclerosis. The

```

CC genes are useful for developing screening assays to screen for compounds  
 CC that regulate the expression of genes associated with cholesterol  
 CC transport. The genes and proteins are also useful for are also useful  
 CC as diagnostic indicators of cardiovascular disease and other disorders  
 CC associated with hypercholesterolemia.

XX Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 48.4%; Score 77; DB 22; Length 10474;  
 Best Local Similarity 99.2%; Pred. No. 5e-29;  
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 agcttgccgctgctccagggctcccgagccacagctggcgctgctgagggg 91

Db 261 agcttgccgctgctccagggctcccgagccacagctggcgctgagggg 320

QY 92 acatggcatgttgccctcagctgaggtgctgctggaagaccccttcacagaagaa 151

Db 321 acatggctgttgccctcagctgaggtgctgctggaagaccccttcacagaagaa 380

QY 152 gacaaaca 159

Db 381 gacaaaca 388

RESULT 7

AAS04035  
 ID AAS04035 standard; cDNA; 446 BP.

XX AAS04035;

DT 12-SEP-2001 (first entry)

XX Partial human ABC1 cDNA sequence.

XX Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
 KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
 KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 185..438

FT /\*tag= a

FT /product= "Human ABC1 protein, amino acids 1 to 60"

XX WO200130848-A2.

XX 03-MAY-2001.

PF 26-OCT-2000; 2000WO-EP10886.

XX 26-OCT-1999; 99EP-0402668.

PR 01-MAR-2000; 2000US-0186260.

XX (AVET ) AVENTIS PHARMA SA.

XX Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;  
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
 PI Dean M;

XX WPI; 2001-316327/33.

DR P-PSDB; AAU02116.

XX New human ABC1 nucleic acids and polypeptides for treating

PT atherosclerosis, malaria and diabetes -

XX Example 2; Page 167; 368pp; English.

XX The sequence represents the partial coding sequence of human ABC1,  
 CC which encodes amino acids 1-60 of the human ABC1 protein. The nucleic  
 CC acid sequence, primers and probes derived from the ABC1 sequence, and

CC polypeptides and vectors are useful for the prevention of  
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse  
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is  
 CC useful for screening for an active ingredient for the prevention or  
 CC treatment of a disease resulting from dysfunction in the reverse  
 CC transport of cholesterol. The nucleic acids and polypeptides are also  
 CC useful for treating and preventing cardiovascular and neurological  
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-  
 CC cholesterol (LCAT) deficiency, malaria and diabetes.

XX Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;

Query Match 37.7%; Score 60; DB 22; Length 446;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tttggctcagctgaggtgctgctggaagaccccttcacagaagacaaca 159

Db 191 tttggctcagctgaggtgctgctggaagaccccttcacagaagacaaca 250

RESULT 8

ABA09200

ID ABA09200 standard; cDNA; 7086 BP.

XX ABA09200;

DT 11-JAN-2002 (first entry)

XX Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder; immune disorder;  
 KW tissue regeneration; wound healing; infection; antiinflammatory;  
 KW cell culture; drug screening; gene therapy; antiarteriosclerotic;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer; ss.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US03800.

XX 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457740/49.

DR P-PSDB; ABB11956.

XX Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -

XX Claim 1; Page 833-835; 1963pp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth factor activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC auto-immune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention.

SQ Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

Query Match 37.7%; Score 60; DB 22; Length 7086;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tgttgccctcagctgaggttgcgtgctggtggaagaacctcactttcagaagaacaaaca 159  
 |||||  
 Db 310 tgttgccctcagctgaggttgcgtgctggtggaagaacctcactttcagaagaacaaaca 369

RESULT 9  
 AAK52667  
 ID AAK52667 standard; cDNA; 7086 BP.  
 AC AAK52667;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 2196.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.

OS Homo sapiens.  
 XX  
 PN WO200157190-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US04098.

XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.  
 PR 01-SEP-2000; 2000US-0654936.  
 PR 15-SEP-2000; 2000US-0663561.  
 PR 20-OCT-2000; 2000US-0693325.  
 PR 30-NOV-2000; 2000US-0728422.  
 XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
 PI Zhao OA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX  
 DR WPI; 2001-476283/51.  
 DR P-PSDB; AAM79534.

XX Nucleic acids encoding polypeptides with cytokine-like activities,  
 PT useful in diagnosis and gene therapy -

XX Claim 1; Page 4558-4560; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAM80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.

XX Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

Query Match 37.7%; Score 60; DB 22; Length 7086;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 tgttgccctcagctgaggttgcgtgctggtggaagaacctcactttcagaagaacaaaca 159  
 |||||  
 Db 310 tgttgccctcagctgaggttgcgtgctggtggaagaacctcactttcagaagaacaaaca 369

RESULT 10  
 AAD21326  
 ID AAD21326 standard; DNA; 7260 BP.  
 XX  
 AC AAD21326;  
 XX  
 DT 28-JAN-2002 (first entry)  
 XX  
 DE Human ATP binding cassette transporter 1 (ABCI) gene.

XX Human; ATP binding cassette transporter 1; ABC1; coronary heart disease;  
 KW dermatological; atherosclerosis; cardiovascular; inflammatory disease;  
 KW psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;  
 KW immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.

OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 321..7106  
 FT CDS /\*tag= a  
 FT /product= "Human ABC1 protein"  
 XX  
 XX EP1136552-A1.  
 XX  
 PD 26-SEP-2001.





SQ Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;

Query Match 37.7%; Score 60; DB 21; Length 7857;  
Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 ttttgccctcagctgaggttgcgtgtggaagaaccttcactttcagaagaagacaaca 159  
|||||  
Db 81 ttttgccctcagctgaggttgcgtgtggaagaaccttcactttcagaagaagacaaca 140  
|||||

## RESULT 14

AAF83826

ID AAF83826 standard; DNA; 7860 BP.

XX AC AAF83826;

XX DT 06-AUG-2001 (first entry)

XX DE Human ABC1 nucleotide sequence.

XX KW ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;  
XX KW LDL; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 75..3341

XX FT /\*tag= a

XX FT /product= "partial ABC1 protein"

XX FT /note= "the coding sequence continues beyond nucleotide  
3341, possibly till position 6860 as identified  
by translating the present sequence; part of the  
corresponding protein is missing and nucleotide  
3341 corresponds to the last amino acid residue  
(position 1089) as indicated in the  
specification"

XX PN WO200132184-A2.

XX PD 10-MAY-2001.

XX PF 01-NOV-2000; 2000WO-US30109.

XX PR 01-NOV-1999; 99US-0162803.

XX PR 30-JUN-2000; 2000US-0215564.

XX XX (WISC ) WISCONSIN ALUMNI RES FOUND.

XX PI Attie AD, Cook M, Gray-Keller MP, Hayden MR, Pimstone S;

XX PI Brooks-Wilson A;

XX XX WPI; 2001-335779/35.

XX DR P-PSDB; AAB62691.

XX XX New method for inhibiting cholesterol uptake in the gut comprises

XX PT administration of an inhibitor of an ABC1 protein

XX PS Disclosure; Page 34-36; 41pp; English.

XX CC The invention relates to a new method for inhibiting cholesterol uptake  
XX CC in the gut that comprises administration of an inhibitor of an ABC1  
XX CC protein. The method is useful for: lowering levels of LDL (low density  
XX CC lipoprotein) cholesterol by reducing the activity of ABC1 protein in the  
XX CC intestinal cells and the abundance of the ABC1 protein in the individual  
XX CC by inhibiting the activity of the protein; identifying drugs that can  
XX CC lower serum cholesterol and LDL levels comprises assaying the drug to  
XX CC test if it can bind to an ABC1 protein; testing LDL cholesterol lowering  
XX CC agents; and for modulation of ABC1 biological activity. The present  
XX CC sequence represents a human ABC1 nucleotide sequence.

XX SQ Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;

Query Match 37.7%; Score 60; DB 22; Length 7860;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 ttttgccctcagctgaggttgcgtgtggaagaaccttcactttcagaagaagacaaca 159  
|||||

Db 81 ttttgccctcagctgaggttgcgtgtggaagaaccttcactttcagaagaagacaaca 140  
|||||

## RESULT 15

AAF92835

ID AAF92835 standard; DNA; 7860 BP.

XX AC AAF92835;

XX DT 17-MAY-2001 (first entry)

XX DE Human ABC1 cDNA.

XX KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ss.

XX OS Homo sapiens.

XX PN WO200115676-A2.

XX PD 08-MAR-2001.

XX PF 01-SEP-2000; 2000WO-IB01492.

XX PR 01-SEP-1999; 99US-0151977.

XX PR 15-MAR-2000; 2000US-0526193.

XX PR 23-JUN-2000; 2000US-0213958.

XX XX (UYBR-) UNIV BRITISH COLUMBIA.

XX PA (XENO-) XENON GENETICS INC.

XX PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;

XX DR WPI; 2001-244356/25.

XX XX Treating a lower than normal high density lipoprotein-cholesterol  
XX PT (HDL-C) level, a higher than normal triglyceride level, or a  
XX PT cardiovascular disease, by administering a compound that modulates LXR-  
XX PT or RXR-mediated transcriptional activity -

XX PS Disclosure; Fig 2; 317pp; English.

XX CC The present invention relates to a method for treating a patient  
XX CC diagnosed as having a lower than normal high density  
XX CC lipoprotein-cholesterol (HDL-C) level, a higher than normal  
XX CC triglyceride level, or a cardiovascular disease, involving  
XX CC administering a compound that modulates LXR- or RXR-mediated  
XX CC transcriptional activity or ABC1 expression or activity.

XX CC The LXR gene product may be used in an assay to identify  
XX CC compounds useful for the treatment of a disease or condition selected a  
XX CC lower than normal HDL cholesterol level, a higher than normal  
XX CC triglyceride level, and a cardiovascular disease.

XX SQ Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other;

## Query Match

Best Local Similarity 37.7%; Score 60; DB 22; Length 7860;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 ttttgccctcagctgaggttgcgtgtggaagaaccttcactttcagaagaagacaaca 159  
|||||

Db 81 ttttgccctcagctgaggttgcgtgtggaagaaccttcactttcagaagaagacaaca 140  
|||||

## RESULT 16

AAC69387  
 ID AAC69387 standard; cDNA; 7861 BP.  
 XX  
 AC AAC69387;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 cholesterol transporter FHA-1 mutant cDNA (delta 2151-2153).  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.  
 OS Homo sapiens.  
 XX  
 XX WO200055318-A2.  
 PN  
 XX 21-SEP-2000.  
 PD  
 XX 15-MAR-2000; 2000WO-IB00532.  
 PF  
 XX 15-MAR-1999; 99US-0124702.  
 PR 08-JUN-1999; 99US-0138048.  
 PR 17-JUN-1999; 99US-0139600.  
 PR 01-SEP-1999; 99US-0151977.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Willson AR, Pimstone SN;  
 PI WPI; 2000-587528/55.  
 DR P-PSDB; AAB38106.  
 DR  
 XX  
 XX New ABC1 polypeptide is useful for treating diseases associated with  
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 PT disease and cancer -  
 PT  
 XX Examples; Page -: 229pp; English.  
 PS  
 CC The invention relates to the human ABC1 cholesterol transporter protein  
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
 CC proteins, and plays a crucial role in cholesterol transport, particularly  
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 CC located on chromosome 9q31, and mutations in this gene are associated  
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary restenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds.  
 CC It further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 CC or prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary restenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated

CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
 CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol  
 CC transporter associated with an altered cholesterol level and therefore an  
 CC altered risk of cardiovascular disease.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the native human ABC1 cDNA shown on pages 157-160.  
 XX  
 XX Sequence 7861 BP; 2014 A; 1859 C; 2011 G; 1976 T; 1 other:  
 SQ  
 Query Match 37.7%; Score 60; DB 21; Length 7861;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 ttttgccctcagctgaggttgctgtgtggaagaacctcactttcagaagaagacaaca 159  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 81 ttttgccctcagctgaggttgctgtgtggaagaacctcactttcagaagaagacaaca 140  
 RESULT 17  
 AAC69120  
 ID AAC69120 standard; cDNA; 7864 BP.  
 XX  
 AC AAC69120;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 XX Human ABC1 cholesterol transporter cDNA.  
 DE  
 XX Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200055318-A2.  
 PN  
 XX 21-SEP-2000.  
 PD  
 XX 15-MAR-2000; 2000WO-IB00532.  
 PF  
 XX 15-MAR-1999; 99US-0124702.  
 PR 08-JUN-1999; 99US-0138048.  
 PR 17-JUN-1999; 99US-0139600.  
 PR 01-SEP-1999; 99US-0151977.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Willson AR, Pimstone SN;  
 PI WPI; 2000-587528/55.  
 DR P-PSDB; AAB38082.  
 DR  
 XX New ABC1 polypeptide is useful for treating diseases associated with  
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 PT disease and cancer -  
 PT  
 XX Claim 13; Page 157-160; 229pp; English.  
 PS  
 XX The invention relates to the human ABC1 cholesterol transporter protein  
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
 CC proteins, and plays a crucial role in cholesterol transport, particularly  
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 CC located on chromosome 9q31, and mutations in this gene are associated  
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary restenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds.  
 CC It further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 CC or prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary restenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated

intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acid, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: A012376.1. The present sequence represents cDNA encoding the human ABC1 cholesterol transporter.

Sequence 7864 BP; 2014 A; 1860 C; 2011 G; 1978 T; 1 other;

Query Match 37.7%; Score 60; DB 21; Length 7864;  
Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 ttgtggcctcagctgaggtgctgctgtggaagacctcactttcagaagaacaaca 159  
|||||

DB 81 ttgtggcctcagctgaggtgctgctgtggaagacctcactttcagaagaacaaca 140  
|||||

## RESULT 18

AAC69385

ID AAC69385 standard; cDNA; 7864 BP.

XX AAC69385;

XX 29-JAN-2001 (first entry)

XX Human ABC1 cholesterol transporter TD-1 mutant cDNA (T4503C).

XX Human ABC1 cholesterol transporter; chromosome 9q31;

KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;

KW cardiovascular disease; coronary artery disease; coronary restenosis;

KW cerebrovascular disease; peripheral vascular disease;

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.

XX Homo sapiens.

XX WO20005318-A2.

PN 21-SEP-2000.

PD 15-MAR-2000; 2000WO-IB00532.

XX 15-MAR-1999; 99US-0124702.

XX 08-JUN-1999; 99US-0138048.

PR

PR

PR 17-JUN-1999; 99US-0139600.

PR 01-SEP-1999; 99US-0151977.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (XENO-) XENON BIORESEARCH INC.

XX Hayden MR, Willson AR, Pimstone SN;

XX WPI; 2000-587528/55.

DR P-PSDB; AAB38104.

XX New ABC1 polypeptide is useful for treating diseases associated with

PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

PT disease and cancer

PS Examples; Page -; 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein

CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is

CC a member of the ATP-binding cassette (ABC transporter) superfamily of

CC proteins, and plays a crucial role in cholesterol transport, particularly

CC intracellular cholesterol trafficking in monocytes and fibroblasts, being

CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is

CC located on chromosome 9q31, and mutations in this gene are associated

CC with two genetic HDL (high density lipoprotein) deficiency disorders,

CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases

CC are distinguishable in that TD is an autosomal recessive disorder, while

CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good

CC cholesterol") in the blood correlate with a high risk of cardiovascular

CC disease, particularly coronary artery disease, but also cerebrovascular

CC disease, coronary restenosis, and peripheral vascular disease.

CC Conversely, a high level of HDL has protective effects against

CC cardiovascular disease. The invention provides genetic constructs and

CC transgenic cells and non-human animals comprising human ABC1 nucleic

CC acids, and methods of gene therapy for the treatment or prevention of

CC cardiovascular disease comprising the administration of an expression

CC vector encoding ABC1 or an active fragment thereof. The invention also

CC encompasses compounds which mimic ABC1 activity, compounds which

CC stimulate ABC1 expression and methods of screening for such compounds.

CC It further relates to methods for determining whether a patient has an

CC increased risk for cardiovascular disease due to polymorphisms in the

CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat

CC or prevent cardiovascular disease, especially coronary artery disease,

CC cerebrovascular disease, coronary restenosis or peripheral vascular

CC disease. They may also be used in the treatment of diseases associated

CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick

CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

CC The invention specifically excludes proteins with the exact amino acid

CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic

CC acid with the exact sequence as GenBank Accession No: A012376.1. The

CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol

CC transporter associated with an altered cholesterol level and therefore an

CC altered risk of cardiovascular disease.

CC Note: The present sequence is not shown in the specification, but is

CC derived from the native human ABC1 cDNA shown on pages 157-160.

XX Sequence 7864 BP; 2014 A; 1861 C; 2011 G; 1977 T; 1 other;

SQ

Query Match 37.7%; Score 60; DB 21; Length 7864;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 ttgtggcctcagctgaggtgctgctgtggaagacctcactttcagaagaacaaca 159

|||||

DB 81 ttgtggcctcagctgaggtgctgctgtggaagacctcactttcagaagaacaaca 140

|||||

## RESULT 19

AAC69386

ID AAC69386 standard; cDNA; 7864 BP.

XX AAC69386;

29-JAN-2001 (first entry)  
 Human ABC1 cholesterol transporter TD-2 mutant cDNA (A1864G).  
 Human ABC1 cholesterol transporter; chromosome 9q31;  
 ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 cardiovascular disease; coronary artery disease; coronary restenosis;  
 cerebrovascular disease; peripheral vascular disease;  
 Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.  
 Homo sapiens.  
 WO200055318-A2.  
 21-SEP-2000.  
 15-MAR-2000; 2000WO-IB00532.  
 15-MAR-1999; 99US-0124702.  
 08-JUN-1999; 99US-0138048.  
 17-JUN-1999; 99US-0139600.  
 01-SEP-1999; 99US-0151977.  
 (UYBR-) UNIV BRITISH COLUMBIA.  
 (XENO-) XENON BIORESEARCH INC.  
 Hayden MR, Wilson AR, Pimstone SN;  
 WPI; 2000-587528/55.  
 P-PSDB; AAB38105.  
 New ABC1 polypeptide is useful for treating diseases associated with  
 ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 disease and cancer -  
 Examples; Page -: 229pp; English.  
 The invention relates to the human ABC1 cholesterol transporter protein  
 (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
 a member of the ATP-binding cassette (ABC transporter) superfamily of  
 proteins, and plays a crucial role in cholesterol transport, particularly  
 intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 located on chromosome 9q31, and mutations in this gene are associated  
 with two genetic HDL (high density lipoprotein) deficiency disorders,  
 Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 are distinguishable in that TD is an autosomal recessive disorder, while  
 FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 cholesterol") in the blood correlate with a high risk of cardiovascular  
 disease, particularly coronary artery disease, but also cerebrovascular  
 disease, coronary restenosis, and peripheral vascular disease.  
 Conversely, a high level of HDL has protective effects against  
 cardiovascular disease. The invention provides genetic constructs and  
 transgenic cells and non-human animals comprising human ABC1 nucleic  
 acids, and methods of gene therapy for the treatment or prevention of  
 cardiovascular disease comprising the administration of an expression  
 vector encoding ABC1 or an active fragment thereof. The invention also  
 encompasses compounds which mimic ABC1 activity, compounds which  
 stimulate ABC1 expression and methods of screening for such compounds.  
 It further relates to methods for determining whether a patient has an  
 increased risk for cardiovascular disease due to polymorphisms in the  
 ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 or prevent cardiovascular disease, especially coronary artery disease,  
 cerebrovascular disease, coronary restenosis or peripheral vascular  
 disease. They may also be used in the treatment of diseases associated  
 with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 The invention specifically excludes proteins with the exact amino acid  
 sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic

CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
 CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol  
 CC transporter associated with an altered cholesterol level and therefore an  
 CC altered risk of cardiovascular disease.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the native human ABC1 cDNA shown on pages 157-160.  
 XX  
 SQ Sequence 7864 BP; 2013 A; 1860 C; 2012 G; 1978 T; 1 other;  
 Query Match 37.7%; Score 60; DB 21; Length 7864;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 ttttgccctcagctgaggttgctgctgtggaagaacctcactttcagaagaacaaca 159  
 Db 81 ttttgccctcagctgaggttgctgctgtggaagaacctcactttcagaagaacaaca 140  
 RESULT 20  
 AAC69389  
 ID AAC69389 standard; cDNA; 7864 BP.  
 XX  
 AC AAC69389;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 cholesterol transporter FHA-2 mutant cDNA (C6504T).  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200055318-A2.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 15-MAR-2000; 2000WO-IB00532.  
 XX  
 PR 15-MAR-1999; 99US-0124702.  
 PR 08-JUN-1999; 99US-0138048.  
 PR 17-JUN-1999; 99US-0139600.  
 PR 01-SEP-1999; 99US-0151977.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON BIORESEARCH INC.  
 PI Hayden MR, Wilson AR, Pimstone SN;  
 XX  
 DR WPI; 2000-587528/55.  
 DR P-PSDB; AAB38105.  
 XX  
 PT New ABC1 polypeptide is useful for treating diseases associated with  
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 PT disease and cancer -  
 PS Examples; Page -: 229pp; English.  
 XX  
 CC The invention relates to the human ABC1 cholesterol transporter protein  
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
 CC proteins, and plays a crucial role in cholesterol transport, particularly  
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 CC located on chromosome 9q31, and mutations in this gene are associated  
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary restenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds.  
 CC It further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 CC or prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary restenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated  
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic

CC Tangler disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary stenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds.  
 CC It further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 CC or prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary stenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated  
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
 CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol  
 CC transporter associated with an altered cholesterol level and therefore an  
 CC altered risk of cardiovascular disease.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the native human ABC1 cDNA shown on pages 157-160.  
 XX  
 SQ Sequence 7864 BP; 2014 A; 1859 C; 2011 G; 1979 T; 1 other;

Query Match 37.7%; Score 60; DB 21; Length 7864;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 tttggcctcagctgaggtgctgtggaagaacctcactttcagaagaacaaca 159  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 81 tttggcctcagctgaggtgctgtggaagaacctcactttcagaagaacaaca 140

RESULT 21  
 AAS06120  
 ID AAS06120 standard; cDNA; 9741 BP.  
 XX  
 AC AAS06120;  
 XX  
 DT 12-SEP-2001 (first entry)  
 DE Human ABC1 DNA sequence #1.  
 XX  
 KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
 KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
 KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 185..6967  
 FT /\*tag= a  
 FT /product= "Human ABC1 protein"  
 XX  
 PN WO200130848-A2.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000WO-EP10886.  
 XX  
 PR 26-OCT-1999; 99EP-0402668.  
 PD 01-MAR-2000; 2000US-0186260.  
 XX  
 PA (AVET ) AVENTIS PHARMA SA.  
 XX  
 PI Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;  
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
 PI Dean M;

PA (AVET ) AVENTIS PHARMA SA.  
 XX  
 PI Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;  
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
 PI Dean M;  
 XX  
 WPI; 2001-316327/33.  
 DR P-PSDB; AAU02176.  
 DR  
 PT New human ABC1 nucleic acids and polypeptides for treating  
 FT atherosclerosis, malaria and diabetes  
 XX  
 PS Claim 1; Page 204-208; 368pp; English.  
 XX  
 CC The sequence represents the coding sequence #1 of human ABC1. The  
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,  
 CC and polypeptides and vectors are useful for the prevention of  
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse  
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is  
 CC useful for screening for an active ingredient for the prevention or  
 CC treatment of a disease resulting from dysfunction in the reverse  
 CC transport of cholesterol. The nucleic acids and polypeptides are also  
 CC useful for treating and preventing cardiovascular and neurological  
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-  
 CC cholesterol (LCAT) deficiency, malaria and diabetes.  
 XX  
 SQ Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;

Query Match 37.7%; Score 60; DB 22; Length 9741;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 tttggcctcagctgaggtgctgtggaagaacctcactttcagaagaacaaca 159  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 191 tttggcctcagctgaggtgctgtggaagaacctcactttcagaagaacaaca 250

RESULT 22  
 AAS06121  
 ID AAS06121 standard; cDNA; 9854 BP.  
 XX  
 AC AAS06121;  
 XX  
 DT 12-SEP-2001 (first entry)  
 DE Human ABC1 DNA sequence #2.  
 XX  
 KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
 KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
 KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 298..7078  
 FT /\*tag= a  
 FT /product= "Human ABC1 protein"  
 XX  
 PN WO200130848-A2.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000WO-EP10886.  
 XX  
 PR 26-OCT-1999; 99EP-0402668.  
 PD 01-MAR-2000; 2000US-0186260.  
 XX  
 PA (AVET ) AVENTIS PHARMA SA.  
 XX  
 PI Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;  
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
 PI Dean M;

XX WPI; 2001-316327/33.  
 DR P-PSDB; AAU02176.  
 XX  
 XX New human ABC1 nucleic acids and polypeptides for treating  
 PT atherosclerosis, malaria and diabetes -  
 XX  
 XX Claim 1; Page 209-213; 368pp; English.  
 XX  
 XX The sequence represents the coding sequence #2 of human ABC1. The  
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,  
 CC and polypeptides and vectors are useful for the prevention of  
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse  
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is  
 CC useful for screening for an active ingredient for the prevention or  
 CC treatment of a disease resulting from dysfunction in the reverse  
 CC transport of cholesterol. The nucleic acids and polypeptides are also  
 CC useful for treating and preventing cardiovascular and neurological  
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-  
 CC cholesterol (LCAT) deficiency, malaria and diabetes.  
 XX  
 XX Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;  
 SQ  
 Query Match 37.7%; Score 60; DB 22; Length 9854;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 tttggcctcagctgaggttgcctgtggaagaacctcacttcagagaagacaaca 159  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 304 tttggcctcagctgaggttgcctgtggaagaacctcacttcagagaagacaaca 363  
 RESULT 23  
 AAC69132  
 ID AAC69132 standard; DNA; 10545 BP.  
 XX  
 AC AAC69132;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 XX Human ABC1 gene exon 1 (promoter).  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31; promoter;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary stenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200055318-A2.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-IB00532.  
 XX  
 XX 15-MAR-1999; 99US-0124702.  
 PR 08-JUN-1999; 99US-0138048.  
 PR 17-JUN-1999; 99US-0139600.  
 PR 01-SEP-1999; 99US-0151977.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Wilson AR, Pimstone SN;  
 PI  
 XX WPI; 2000-587528/55.  
 DR  
 XX New ABC1 polypeptide is useful for treating diseases associated with

PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 PT disease and cancer -  
 XX  
 PS Claim 50; Fig 12; 229pp; English.  
 XX  
 XX The invention relates to the human ABC1 cholesterol transporter protein  
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
 CC proteins, and plays a crucial role in cholesterol transport, particularly  
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 CC located on chromosome 9q31, and mutations in this gene are associated  
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary stenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds.  
 CC It further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 CC or prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary stenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated  
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
 CC present sequence represents the human ABC1 gene promoter region (exon 1).  
 XX  
 SQ Sequence 10545 BP; 2647 A; 2225 C; 2411 G; 3256 T; 6 other;  
 Query Match 37.7%; Score 60; DB 21; Length 10545;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 tttggcctcagctgaggttgcctgtggaagaacctcacttcagagaagacaaca 159  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 8240 tttggcctcagctgaggttgcctgtggaagaacctcacttcagagaagacaaca 8299  
 RESULT 24  
 AAF92831  
 ID AAF92831 standard; DNA; 183999 BP.  
 XX  
 AC AAF92831;  
 XX  
 DT 17-MAY-2001 (first entry)  
 XX  
 DE Human ABC1 genomic DNA.  
 XX  
 XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200115676-A2.  
 PN  
 XX 08-MAR-2001.  
 PD  
 XX 01-SEP-2000; 2000WO-IB01492.  
 PF  
 XX 01-SEP-1999; 99US-0151977.  
 PR

```
PR 15-MAR-2000; 2000US-0526193.
PR 23-JUN-2000; 2000US-0213958.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON GENETICS INC.
XX
XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX WPT; 2001-244356/25.
XX
XX Treating a lower than normal high density lipoprotein-cholesterol
XX (HDL-C) level, a higher than normal triglyceride level, or a
XX cardiovascular disease, by administering a compound that modulates LXR-
XX or RXR-mediated transcriptional activity -
XX
XX Claim 8; Fig 1; 317pp; English.
XX
XX The present invention relates to a method for treating a patient
XX diagnosed as having a lower than normal high density
XX lipoprotein-cholesterol (HDL-C) level, a higher than normal
XX triglyceride level, or a cardiovascular disease, involving
XX administering a compound that modulates LXR- or RXR-mediated
XX transcriptional activity or ABC1 expression or activity.
XX The LXR gene product may be used in an assay to identify
XX compounds useful for the treatment of a disease or condition selected a
XX lower than normal HDL cholesterol level, a higher than normal
XX triglyceride level, and a cardiovascular disease.
XX
XX Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
XX
XX Query Match 37.7%; Score 60; DB 22; Length 183999;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-20;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 100 ttgtgctcagctgaggtgctgctgtggaagaacctcactttcagaagaagacaaaca 159
XX |||||||
XX Db 53328 ttgtgctcagctgaggtgctgctgtggaagaacctcactttcagaagaagacaaaca 53387
XX |||||||
XX
XX RESULT 25
XX AAH07432
XX ID AAH07432 standard; cDNA: 736 BP.
XX
XX AC AAH07432;
XX
XX DT 26-JUN-2001 (first entry)
XX
XX DE Human cDNA clone (5'-primer) SEQ ID NO:4267.
XX
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1074617-A2.
XX
XX PD 07-FEB-2001.
XX
XX PF 28-JUL-2000; 2000EP-0116126.
XX
XX PR 29-JUL-1999; 99JP-0248036.
XX PR 27-AUG-1999; 99JP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
XX AAB98993 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
XX
XX Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;
XX
XX Query Match 32.1%; Score 51; DB 22; Length 736;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-16;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 109 cagctgaggtgctgctgtggaagaacctcactttcagaagaagacaaaca 159
XX |||||||
XX Db 329 cagctgaggtgctgctgtggaagaacctcactttcagaagaagacaaaca 379
XX |||||||
XX
XX RESULT 26
XX AAH18606
XX ID AAH18606 standard; cDNA: 1556 BP.
XX
XX AC AAH18606;
XX
XX DT 26-JUN-2001 (first entry)
XX
XX DE Human cDNA sequence SEQ ID NO:18808.
XX
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1074617-A2.
XX
XX PD 07-FEB-2001.
XX
XX PF 28-JUL-2000; 2000EP-0116126.
XX
XX PR 29-JUL-1999; 99JP-0248036.
XX PR 27-AUG-1999; 99JP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
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DR WPT; 2001-318749/34.  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 8; SEQ ID 18808; 2537pp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX  
 SQ Sequence 1556 BP; 380 A; 363 C; 399 G; 414 T; 0 other;

Query Match 32.1%; Score 51; DB 22; Length 1556;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-16;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 109 cagctgaggttgcgtgtggaagaacctcactttcagaagaagacaaca 159  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 329 cagctgaggttgcgtgtggaagaacctcactttcagaagaagacaaca 379

RESULT 27  
 AAF93084  
 ID AAF93084 standard; DNA; 37 BP.  
 AC AAF93084;  
 XX  
 DT 17-MAY-2001 (first entry)  
 XX  
 DE ABC1 polymorphism RFLP oligonucleotide #45.  
 XX  
 KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200115676-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 01-SEP-2000; 2000WO-IB01492.  
 XX  
 PR 01-SEP-1999; 99US-0151977.  
 PR 15-MAR-2000; 2000US-0526193.  
 PR 23-JUN-2000; 2000US-0213958.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON GENETICS INC.  
 XX  
 PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;  
 XX  
 XX

DR WPI; 2001-244356/25.  
 XX  
 PT Treating a lower than normal high density lipoprotein-cholesterol  
 PT (HDL-C) level, a higher than normal triglyceride level, or a  
 PT cardiovascular disease, by administering a compound that modulates LXR-  
 PT or RXR-mediated transcriptional activity -  
 XX  
 PS Disclosure; Fig 17; 317pp; English.  
 XX  
 CC The present invention relates to a method for treating a patient  
 CC diagnosed as having a lower than normal high density  
 CC lipoprotein-cholesterol (HDL-C) level, a higher than normal  
 CC triglyceride level, or a cardiovascular disease, involving  
 CC administering a compound that modulates LXR- or RXR-mediated  
 CC transcriptional activity or ABC1 expression or activity.  
 CC The LXR gene product may be used in an assay to identify  
 CC compounds useful for the treatment of a disease or condition selected a  
 CC lower than normal HDL cholesterol level, a higher than normal  
 CC triglyceride level, and a cardiovascular disease.  
 XX  
 SQ Sequence 37 BP; 4 A; 17 C; 11 G; 5 T; 0 other;

Query Match 22.0%; Score 35; DB 22; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-08;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 39 gccgcgtccttcacaggtcccgagccacacgctg 73  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 1 gccgcgtccttcacaggtcccgagccacacgctg 35

RESULT 28  
 AAC69306  
 ID AAC69306 standard; DNA; 21 BP.  
 XX  
 AC AAC69306;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 gene promoter polymorphic site, SEQ ID NO:205.  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055318-A2.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 15-MAR-2000; 2000WO-IB00532.  
 XX  
 PR 15-MAR-1999; 99US-0124702.  
 PR 08-JUN-1999; 99US-0138048.  
 PR 17-JUN-1999; 99US-0139600.  
 PR 01-SEP-1999; 99US-0151977.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON BIORESEARCH INC.  
 XX  
 PI Hayden MR, Wilson AR, Pimstone SN;  
 XX  
 XX WPI; 2000-587528/55.  
 XX  
 XX New ABC1 polypeptide is useful for treating diseases associated with  
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

PT disease and cancer -

PS Examples; Fig 11; 229pp; English.

XX

CC The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a polymorphic site of the human ABC1 gene.

XX Sequence 21 BP; 2 A; 6 C; 9 G; 4 T; 0 other;

SQ

Query Match 13.2%; Score 21; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 acacgctggcgctgctgctg 86

DB 1 acacgctggcgctgctgctg 21

|||||

RESULT 29

AAC69308

ID AAC69308 standard; DNA; 21 BP.

XX

AC AAC69308;

XX

DT 29-JAN-2001 (first entry)

XX

DE Human ABC1 gene promoter polymorphic site, SEQ ID NO:207.

XX

KW Human ABC1 cholesterol transporter; chromosome 9q31;

KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;

KW cerebrovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease;

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prognosis; prophylaxis; drug screening; transgenic animal; ds.

XX Homo sapiens.

OS

PN WO200055318-A2.

XX

PD 21-SEP-2000.

XX

PF 15-MAR-2000; 2000WO-IB00532.

XX

PR 15-MAR-1999; 99US-0124702.

PR 08-JUN-1999; 99US-0138048.

PR 17-JUN-1999; 99US-0139600.

PR 01-SEP-1999; 99US-0151977.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

PA (XENO-) XENON BIORESEARCH INC.

XX

PI Hayden MR, Wilson AR, Pimstone SN;

PI WPI; 2000-587528/55.

DR

XX New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and cancer -

PT

PT Examples; Fig 11; 229pp; English.

PS

XX The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a polymorphic site of the human ABC1 gene.

XX Sequence 21 BP; 2 A; 6 C; 9 G; 4 T; 0 other;

SQ

Query Match 13.2%; Score 21; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 acacgctggcgctgctgctg 86

DB 1 acacgctggcgctgctgctg 21

|||||

RESULT 29

AAC69308

ID AAC69308 standard; DNA; 21 BP.

XX

AC AAC69308;

XX

DT 29-JAN-2001 (first entry)

XX

DE Human ABC1 gene promoter polymorphic site, SEQ ID NO:207.

XX

KW Human ABC1 cholesterol transporter; chromosome 9q31;

KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;

KW cerebrovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease;

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prognosis; prophylaxis; drug screening; transgenic animal; ds.

XX Homo sapiens.

OS

AAF92946  
ID AAF92946 standard; DNA; 21 BP.  
XX  
AC AAF92946;  
XX  
DT 17-MAY-2001 (first entry)  
XX  
DE Polymorphic sequence for ABC1 polymorphic site #17.  
XX  
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200115676-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 01-SEP-2000; 2000WO-IB01492.  
XX  
PR 01-SEP-1999; 99US-0151977.  
PR 15-MAR-2000; 2000US-0526193.  
PR 23-JUN-2000; 2000US-0213958.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (XENO-) XENON GENETICS INC.  
XX  
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;  
XX  
DR WPI; 2001-244356/25.  
XX  
PT Treating a lower than normal high density lipoprotein-cholesterol  
PT (HDL-C) level, a higher than normal triglyceride level, or a  
PT cardiovascular disease, by administering a compound that modulates LXR-  
PT or RXR-mediated transcriptional activity -  
XX  
PS Disclosure; Fig 4; 317pp; English.  
XX  
CC The present invention relates to a method for treating a patient  
CC diagnosed as having a lower than normal high density  
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal  
CC triglyceride level, or a cardiovascular disease, involving  
CC administering a compound that modulates LXR- or RXR-mediated  
CC transcriptional activity or ABC1 expression or activity.  
CC The LXR gene product may be used in an assay to identify  
CC compounds useful for the treatment of a disease or condition selected a  
CC lower than normal HDL cholesterol level, a higher than normal  
CC triglyceride level, and a cardiovascular disease.  
XX  
SQ Sequence 21 BP; 3 A; 10 C; 6 G; 2 T; 0 other;  
XX  
CC The present invention relates to a method for treating a patient  
CC diagnosed as having a lower than normal high density  
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal  
CC triglyceride level, or a cardiovascular disease, involving  
CC administering a compound that modulates LXR- or RXR-mediated  
CC transcriptional activity or ABC1 expression or activity.  
CC The LXR gene product may be used in an assay to identify  
CC compounds useful for the treatment of a disease or condition selected a  
CC lower than normal HDL cholesterol level, a higher than normal  
CC triglyceride level, and a cardiovascular disease.  
XX  
SQ Sequence 21 BP; 3 A; 10 C; 6 G; 2 T; 0 other;  
XX  
Query Match 13.2%; Score 21; DB 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.56;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 7 accagccacggcgctccctgc 27  
DB 1 accagccacggcgctccctgc 21  
XXXXXXXXXXXXXXXXXXXX  
RESULT 31  
AAF92948  
ID AAF92948 standard; DNA; 21 BP.  
XX  
AC AAF92948;  
XX  
DT 17-MAY-2001 (first entry)  
XX  
DE Polymorphic sequence for ABC1 polymorphic site #18.  
XX  
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.  
XX  
OS Homo sapiens.

XX WO200115676-A2.  
PN  
XX  
PD 08-MAR-2001.  
XX  
PF 01-SEP-2000; 2000WO-IB01492.  
XX  
PR 01-SEP-1999; 99US-0151977.  
PR 15-MAR-2000; 2000US-0526193.  
PR 23-JUN-2000; 2000US-0213958.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (XENO-) XENON GENETICS INC.  
XX  
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;  
XX  
DR WPI; 2001-244356/25.  
XX  
PT Treating a lower than normal high density lipoprotein-cholesterol  
PT (HDL-C) level, a higher than normal triglyceride level, or a  
PT cardiovascular disease, by administering a compound that modulates LXR-  
PT or RXR-mediated transcriptional activity -  
XX  
PS Disclosure; Fig 4; 317pp; English.  
XX  
CC The present invention relates to a method for treating a patient  
CC diagnosed as having a lower than normal high density  
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal  
CC triglyceride level, or a cardiovascular disease, involving  
CC administering a compound that modulates LXR- or RXR-mediated  
CC transcriptional activity or ABC1 expression or activity.  
CC The LXR gene product may be used in an assay to identify  
CC compounds useful for the treatment of a disease or condition selected a  
CC lower than normal HDL cholesterol level, a higher than normal  
CC triglyceride level, and a cardiovascular disease.  
XX  
SQ Sequence 21 BP; 2 A; 6 C; 9 G; 4 T; 0 other;  
XX  
Query Match 13.2%; Score 21; DB 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.56;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 66 acacgctggcgctgcgtgctg 86  
DB 1 acacgctggcgctgcgtgctg 21  
XXXXXXXXXXXXXXXXXXXX  
RESULT 32  
AAA68004  
ID AAA68004 standard; DNA; 577 BP.  
XX  
AC AAA68004;  
XX  
DT 24-OCT-2000 (first entry)  
XX  
DE Pinus radiata PAL nucleotide sequence SEQ ID NO:97.  
XX  
KW Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;  
KW Pinus radiata; Monterey pine; ds.  
XX  
OS Pinus radiata.  
XX  
PN WO200022099-A1.  
XX  
PD 20-APR-2000.  
XX  
PF 06-OCT-1999; 99WO-NZ00168.  
XX  
PR 09-OCT-1998; 98US-0169789.  
PR 14-JUL-1999; 99US-0143811.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 XX  
 PI Bloksberg LN, Havukkala IJ;  
 XX  
 XX WPI; 2000-317962/27.  
 DR  
 XX  
 XX Novel polynucleotide encoding enzymes involved in lignin-biosynthetic  
 PT pathway useful for producing transgenic plants especially eucalyptus  
 PT and pine species having altered lignin content, composition and  
 PT structure -  
 XX  
 XX  
 PS Claim 1; Page 87; 213pp; English.  
 CC  
 CC The present invention describes isolated polynucleotides and proteins  
 CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),  
 CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase  
 CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase  
 CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),  
 CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),  
 CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,  
 CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase,  
 CC coumarate CoA ligase, cytochrome P450 1X1A, diphenol oxidase, flavanol  
 CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase,  
 CC which are involved in the lignin biosynthetic pathway. The  
 CC polynucleotides can be used for modulating lignin content, lignin  
 CC composition and the structure of a plant, especially eucalyptus and pine  
 CC species, and for modifying the activity of an enzyme involved in lignin  
 CC biosynthetic pathway, and for producing a plant having altered lignin  
 CC content, composition and structure. They can be used for designing probes  
 CC and primers useful for detecting similar DNA and RNA sequences in any  
 CC organism and for PCR amplification. The lignin content can be efficiently  
 CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to  
 CC AAB16449 represent polynucleotide and protein sequences used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 577 BP; 128 A; 174 C; 165 G; 110 T; 0 other;  
 SQ

Query Match 11.9%; Score 19; DB 21; Length 577;  
 Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0;

QY 70 gctggcgctgctggctgag 88  
 |||||  
 Db 154 gctggcgctgctggctgag 172

RESULT 33  
 AAV23916  
 ID AAV23916 standard; DNA; 624 BP.  
 XX  
 AC AAV23916;  
 XX  
 XX 31-JUL-1998 (first entry)  
 DT  
 DE Plant PAL enzyme DNA sequence.  
 XX  
 XX Lignin biosynthetic pathway; eucalyptus; pine; transgenic plant;  
 KW Lignin content; tree processing; cellulose fibre; ss.  
 XX  
 OS Pinus radiata.  
 XX  
 XX WO9811205-A2.  
 PN  
 XX 19-MAR-1998.  
 PD  
 XX 10-SEP-1997; 97WO-NZ00112.  
 PF  
 XX 11-SEP-1996; 96US-0713000.  
 PR  
 XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX

PI Bloksberg LN, Grierson AW, Havukkala IJ;  
 XX  
 DR WPI; 1998-207374/18.  
 XX  
 XX Sequences useful for modification of plant lignin content or  
 PT structure - from Eucalyptus grandis (eucalyptus) and Pinus radiata  
 PT (pine) are associated with lignin biosynthesis pathway, useful e.g.  
 PT in paper industry  
 XX  
 XX Example 2; Page 32; 82pp; English.  
 PS  
 CC This sequence represents a fragment of the PAL enzyme coding sequence. It  
 CC is an example of a DNA sequence of the invention, which are from  
 CC Eucalyptus grandis (eucalyptus) and Pinus radiata (pine) associated with  
 CC the lignin biosynthesis pathway. Constructs containing the DNA sequences  
 CC can be used to produce transgenic plants or plant cells, especially woody  
 CC plants e.g. eucalyptus or pine species but also e.g. monocotyledons or  
 CC dicotyledons; by stably incorporating the constructs into the plant  
 CC genome. The lignin content or structure, or activity of a specific enzyme  
 CC in the plant, can therefore be modulated. Reductions in lignin content or  
 CC changes in composition are useful in tree processing for paper. High  
 CC lignin content results in energy- and chemical-intensive separation  
 CC methods in order to obtain the pure cellulose fibre required. Reductions  
 CC in lignin content may also be useful for forage crops, whilst increases  
 CC or changes in composition may be desirable to increase the mechanical  
 CC strength of wood, change its colour or increase its resistance to rot.  
 CC The sequences are also useful as probes to isolate DNA sequences encoding  
 CC enzymes involved in the lignin biosynthesis pathway from other plant  
 CC species.  
 XX  
 SQ Sequence 624 BP; 136 A; 188 C; 188 G; 111 T; 1 other;  
 Query Match 11.9%; Score 19; DB 19; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctggcgctgctggctgag 88  
 |||||  
 Db 261 gctggcgctgctggctgag 279

RESULT 34  
 AAZ06895  
 ID AAZ06895 standard; cDNA; 624 BP.  
 XX  
 AC AAZ06895;  
 XX  
 XX 09-NOV-1999 (first entry)  
 DT  
 XX Pine phenylalanine ammonia-lyase (PAL) partial cDNA 1.  
 DE  
 XX Lignin; biosynthesis; forage crop; wood; paper production;  
 KW transgenic plant; ss.  
 XX  
 OS Pinus radiata.  
 XX  
 XX US9592486-A.  
 PN  
 XX 14-SEP-1999.  
 PD  
 XX 21-NOV-1997; 97US-0975316.  
 PF  
 XX 21-NOV-1997; 97US-0975316.  
 PR  
 XX 11-SEP-1996; 96US-0713000.  
 PR  
 XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 XX Bloksberg LN, Grierson AW, Havukkala I;  
 PI WPI; 1999-527029/44.  
 DR  
 XX

PT Isolated DNA sequence encoding enzymes from the lignin synthetic  
 PT pathway useful for generating plants with an altered lignin content  
 XX  
 PS  
 CC Example 2; Columns 25-26; 48pp; English.  
 CC  
 CC This sequence represents a phenylalanine ammonia-lyase (PAL)  
 CC partial cDNA from *Pinus radiata*. This enzyme is involved in the  
 CC biosynthesis of lignin, an insoluble polymer which is primarily  
 CC responsible for the rigidity of plant stems. Lignin serves as a matrix  
 CC around the polysaccharide components of some plant cell walls. The  
 CC higher the lignin content, the more rigid the plant. Lignin also plays a  
 CC role in disease resistance of plants by impeding the penetration and  
 CC propagation of pathogenic agents. Lignin is formed by polymerisation of  
 CC at least three different monolignols (para-coumaryl alcohol, coniferyl  
 CC alcohol and sinapyl alcohol). These three monolignols are synthesised by  
 CC similar pathways from phenylalanine in a multistep process and are  
 CC believed to be polymerised into lignin via a free radical mechanism.  
 CC The lignin content of plants can be altered using DNA sequences encoding  
 CC these enzymes. Lignin content can be increased by incorporation of  
 CC additional copies of genes encoding these enzymes into the target plant.  
 CC This could be beneficial for increasing the mechanical strength of wood.  
 CC Similarly, a decrease in lignin content can be obtained by transforming  
 CC the target plant with antisense copies of such genes. This may be  
 CC beneficial in plants used as forage crops for livestock (lignin is  
 CC indigestible) and in trees used in paper manufacture.  
 CC  
 XX Sequence 624 BP; 136 A; 188 C; 188 G; 111 T; 1 other;  
 SQ

Query Match 11.9%; Score 19; DB 20; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctggcgctgctgctgag 88  
 |||||  
 Db 261 gctggcgctgctgctgag 279

RESULT 35  
 AAV67916  
 ID AAA67916 standard; DNA; 624 BP.  
 XX  
 AC AAA67916;  
 XX  
 DT 24-OCT-2000 (first entry)  
 XX  
 DE *Pinus radiata* PAL nucleotide sequence SEQ ID NO:9.  
 XX  
 KW Plant; lignin; lignin biosynthetic pathway; *Eucalyptus grandis*;  
 KW *Pinus radiata*; Monterey pine; ds.  
 XX  
 OS *Pinus radiata*.  
 XX  
 PN WO200022099-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 06-OCT-1999; 99WO-NZ00168.  
 XX  
 PR 09-OCT-1998; 98US-0169789.  
 PR 14-JUL-1999; 99US-0143811.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 XX  
 PI Bloksberg LN, Havukkala IJ;  
 XX  
 DR WPI; 2000-317962/27.  
 XX  
 XX Novel polynucleotide encoding enzymes involved in lignin-biosynthetic  
 PT pathway useful for producing transgenic plants especially *eucalyptus*  
 PT and pine species having altered lignin content, composition and  
 PT structure -

XX Example 2; Page 59-60; 213pp; English.  
 XX  
 PS The present invention describes isolated polynucleotides and proteins  
 CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),  
 CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase  
 CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase  
 CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),  
 CC coniferyl glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),  
 CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,  
 CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase,  
 CC coumarate CoA ligase, cytochrome P450 1XX1A, diphenol oxidase, flavanol  
 CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase,  
 CC which are involved in the lignin biosynthetic pathway. The  
 CC polynucleotides can be used for modulating lignin content, lignin  
 CC composition and the structure of a plant, especially *eucalyptus* and pine  
 CC species, and for modifying the activity of an enzyme involved in lignin  
 CC biosynthetic pathway, and for producing a plant having altered lignin  
 CC content, composition and structure. They can be used for designing probes  
 CC and primers useful for detecting similar DNA and RNA sequences in any  
 CC organism and for PCR amplification. The lignin content can be efficiently  
 CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to  
 CC AAB16449 represent polynucleotide and protein sequences used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 624 BP; 136 A; 188 C; 188 G; 111 T; 1 other;

Query Match 11.9%; Score 19; DB 21; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctggcgctgctgctgag 88  
 |||||  
 Db 261 gctggcgctgctgctgag 279

RESULT 36  
 AAV23865  
 ID AAV23865 standard; DNA; 684 BP.  
 XX  
 AC AAV23865;  
 XX  
 DT 31-JUL-1998 (first entry)  
 XX  
 DE Plant PAL enzyme DNA sequence.  
 XX  
 KW Lignin biosynthetic pathway; *eucalyptus*; pine; transgenic plant;  
 KW lignin content; tree processing; cellulose fibre; ss.  
 XX  
 OS *Pinus radiata*.  
 XX  
 PN WO9811205-A2.  
 XX  
 PD 19-MAR-1998.  
 XX  
 PF 10-SEP-1997; 97WO-NZ00112.  
 XX  
 PR 11-SEP-1996; 96US-0713000.  
 XX  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Bloksberg LN, Grierson AW, Havukkala IJ;  
 XX  
 DR WPI; 1998-207374/18.  
 XX  
 XX Sequences useful for modification of plant lignin content or  
 PT structure - from *Eucalyptus grandis* (*eucalyptus*) and *Pinus radiata*  
 PT (pine) are associated with lignin biosynthesis pathway, useful e.g.  
 PT in paper industry  
 XX  
 PS Claim 1; Page 47; 82pp; English.

XX This sequence represents a fragment of the PAL enzyme coding sequence. It  
 CC is an example of a DNA sequence of the invention, which are from  
 CC Eucalyptus grandis (eucalyptus) and Pinus radiata (pine) associated with  
 CC the lignin biosynthesis pathway. Constructs containing the DNA sequences  
 CC can be used to produce transgenic plants or plant cells, especially woody  
 CC plants e.g. eucalyptus or pine species but also e.g. monocotyledons or  
 CC dicotyledons; by stably incorporating the constructs into the plant  
 CC genome. The lignin content or structure, or activity of a specific enzyme  
 CC in the plant, can therefore be modulated. Reductions in lignin content or  
 CC changes in composition are useful in tree processing for paper. High  
 CC lignin content results in energy- and chemical-intensive separation  
 CC methods in order to obtain the pure cellulose fibre required. Reductions  
 CC in lignin content may also be useful for forage crops, whilst increases  
 CC or changes in composition may be desirable to increase the mechanical  
 CC strength of wood, change its colour or increase its resistance to rot.  
 CC The sequences are also useful as probes to isolate DNA sequences encoding  
 CC enzymes involved in the lignin biosynthesis pathway from other plant  
 CC species.

XX Sequence 684 BP; 150 A; 207 C; 200 G; 127 T; 0 other;

Query Match 11.9%; Score 19; DB 19; Length 684;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 gctggcgctgctggctgag 88  
 |||||  
 Db 261 gctggcgctgctggctgag 279

RESULT 37  
 AAZ06898  
 ID AAZ06898 standard; cDNA; 684 BP.

XX AC AAZ06898;  
 XX 09-NOV-1999 (first entry)  
 XX Pine phenylalanine ammonia-lyase (PAL) partial cDNA 4.  
 XX Lignin; biosynthesis; forage crop; wood; paper production;  
 XX transgenic plant; ss.

XX Pinus radiata.

XX US5952486-A.

XX 14-SEP-1999.

XX 21-NOV-1997; 97US-0975316.

XX 21-NOV-1997; 97US-0975316.

XX 11-SEP-1996; 96US-0713000.

XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Bloksberg LN, Grierson AW, Havukkala I;

XX WPI; 1999-527029/44.

XX Isolated DNA sequence encoding enzymes from the lignin synthetic  
 PT pathway useful for generating plants with an altered lignin content

XX Example 2; Columns 49-52; 48pp; English.

XX This sequence represents a phenylalanine ammonia-lyase (PAL)  
 CC partial cDNA from Pinus radiata. This enzyme is involved in the  
 CC biosynthesis of lignin, an insoluble polymer which is primarily  
 CC responsible for the rigidity of plant stems. Lignin serves as a matrix  
 CC around the polysaccharide components of some plant cell walls. The

CC higher the lignin content, the more rigid the plant. Lignin also plays a  
 CC role in disease resistance of plants by impeding the penetration and  
 CC propagation of pathogenic agents. Lignin is formed by polymerisation of  
 CC at least three different monolignols (para-coumaryl alcohol, coniferyl  
 CC alcohol and sinapyl alcohol). These three monolignols are synthesised by  
 CC similar pathways from phenylalanine in a multistep process and are  
 CC believed to be polymerised into lignin via a free radical mechanism.  
 CC The lignin content of plants can be altered using DNA sequences encoding  
 CC these enzymes. Lignin content can be increased by incorporation of  
 CC additional copies of genes encoding these enzymes into the target plant.  
 CC This could be beneficial for increasing the mechanical strength of wood.  
 CC Similarly, a decrease in lignin content can be obtained by transforming  
 CC the target plant with antisense copies of such genes. This may be  
 CC beneficial in plants used as forage crops for livestock (lignin is  
 CC indigestible) and in trees used in paper manufacture.

XX Sequence 684 BP; 150 A; 207 C; 200 G; 127 T; 0 other;

Query Match 11.9%; Score 19; DB 20; Length 684;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 gctggcgctgctggctgag 88  
 |||||  
 Db 261 gctggcgctgctggctgag 279

RESULT 38  
 AAA69586  
 ID AAA69586 standard; cDNA; 684 BP.

XX AC AAA69586;

XX 08-NOV-2000 (first entry)

XX Pinus radiata phenylalanine ammonia-lyase cDNA SEQ ID NO:60.

XX Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;  
 KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;  
 KW genome mapping; physical mapping; positional cloning; forestry;  
 KW agriculture; medicine; fermentation; plant development; pest resistance;  
 KW pinene; myrcene; Monterey pine; ss.

XX Pinus radiata.

XX WO200036081-A2.

XX 22-JUN-2000.

XX 16-DEC-1999; 99WO-N200219.

XX 17-DEC-1998; 98US-0215504.

XX 29-JUL-1999; 99US-0146441.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Havukkala IJ;

XX WPI; 2000-431575/37.

XX New plant polynucleotides encoding polypeptides involved in the  
 PT production and modification of isoprenoids, useful in forestry and  
 PT agriculture for manipulation of isoprenoid metabolism -

XX Example 4; Page 73; 164pp; English.

XX The present invention describes plant polynucleotides encoding  
 CC polypeptides involved in the production and modification of isoprenoids,  
 CC such as terpenoid and steroid compounds. The polynucleotides are used  
 CC in genome mapping, in physical mapping and in positional cloning of  
 CC genes. The polynucleotides and polypeptides are useful in forestry and

CC agriculture for manipulation of isoprenoid metabolism, in medicine for  
 CC therapeutic effects, including direct application in diseased organisms  
 CC or indirect application by transgenic organisms and in fermentation and  
 CC chemical processing industries involving isoprenoids. In plant  
 CC applications, manipulating isoprenoid pathways or isoprenoid composition  
 CC may, for example, affect plant development, pest resistance, and the  
 CC value of extractives (e.g. pinene and myrcene). The ubiquitous and  
 CC varied roles of isoprenoids make the polynucleotides attractive targets  
 CC for biotechnical applications in a variety of fields. AAA69527 to  
 CC AAA69690 and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus  
 CC radiata polynucleotides and proteins used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 684 BP; 150 A; 207 C; 200 G; 127 T; 0 other;

Query Match 11.9%; Score 19; DB 21; Length 684;  
 Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Gaps 0;  
 Matches 19; Conservative 0; Indels 0; Gaps 0;  
 QY 70 gctggcgctgctgctgag 88  
 |||||  
 Db 261 gctggcgctgctgctgag 279

RESULT 39  
 AAA67952  
 ID AAA67952 standard; DNA; 684 BP.  
 XX  
 AC AAA67952;  
 XX  
 DT 24-OCT-2000 (first entry)  
 XX  
 DE Pinus radiata PAL nucleotide sequence SEQ ID NO:45.  
 XX  
 KW Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;  
 KW Pinus radiata; Monterey pine; ds.  
 XX  
 OS Pinus radiata.  
 XX  
 PN WO200022099-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 06-OCT-1999; 99WO-NZ00168.  
 XX  
 PR 09-OCT-1998; 98US-0169789.  
 PR 14-JUL-1999; 99US-0143811.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 XX  
 PI Bloksberg LN, Havukkala IJ;  
 XX  
 DR WPI; 2000-317962/27.  
 XX  
 PT Novel polynucleotide encoding enzymes involved in lignin-biosynthetic  
 PT pathway useful for producing transgenic plants especially eucalyptus  
 PT and pine species having altered lignin content, composition and  
 PT structure.  
 XX  
 PS Example 2; Page 69; 213pp; English.  
 XX

CC The present invention describes isolated polynucleotides and proteins  
 CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),  
 CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase  
 CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase  
 CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),  
 CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),  
 CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,  
 CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase,  
 CC coumarate CoA ligase, cytochrome P450 1X1A, diphenol oxidase, flavanol  
 CC glucosyl transferase, flavanoid hydroxylase, and isoflavone reductase,  
 CC

CC which are involved in the lignin biosynthetic pathway. The  
 CC polynucleotides can be used for modulating lignin content, lignin  
 CC composition and the structure of a plant, especially eucalyptus and pine  
 CC species, and for modifying the activity of an enzyme involved in lignin  
 CC biosynthetic pathway, and for producing a plant having altered lignin  
 CC content, composition and structure. They can be used for designing probes  
 CC and primers useful for detecting similar DNA and RNA sequences in any  
 CC organism and for PCR amplification. The lignin content can be efficiently  
 CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to  
 CC AAB16449 represent polynucleotides and protein sequences used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 684 BP; 150 A; 207 C; 200 G; 127 T; 0 other;

Query Match 11.9%; Score 19; DB 21; Length 684;  
 Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Gaps 0;  
 Matches 19; Conservative 0; Indels 0; Gaps 0;  
 QY 70 gctggcgctgctgctgag 88  
 |||||  
 Db 261 gctggcgctgctgctgag 279

RESULT 40  
 AAS73156  
 ID AAS73156 standard; cDNA; 5286 BP.  
 XX  
 AC AAS73156;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #8960.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG08969.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID No 8960; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 5286 BP; 1786 A; 1178 C; 1073 G; 1249 T; 0 other;

Query Match 11.9%; Score 19; DB 23; Length 5286;  
 Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0;

QY 141 ttccagaagaagacaaaca 159  
 |||||  
 Db 1961 ttccagaagaagacaaaca 1979

RESULT 41  
 AAS80591  
 ID AAS80591 standard; cDNA; 5954 BP.

XX AC AAS80591;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #16395.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG16404.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

XX PS Claim 1; SEQ ID No 16395; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 5954 BP; 2007 A; 1302 C; 1219 G; 1426 T; 0 other;

Query Match 11.9%; Score 19; DB 23; Length 5954;  
 Best Local Similarity 100.0%; Pred. No. 5.8; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0;

QY 141 ttccagaagaagacaaaca 159  
 |||||  
 Db 2104 ttccagaagaagacaaaca 2122

RESULT 42  
 AAS83843/C  
 ID AAS83843 standard; cDNA; 6143 BP.

XX AC AAS83843;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #19647.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG19656.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

XX PS Claim 1; SEQ ID No 19647; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pot\_sequences.  
 XX  
 SQ Sequence 6143 BP; 1489 A; 1251 C; 1342 G; 2061 T; 0 other;  
 Query Match 11.9%; Score 19; DB 23; Length 6143;  
 Best Local Similarity 100.0%; Pred. No. 5.8;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 141 ttccagaagaagacaaaca 159  
 Db 4040 TTTCAGAGAGAGACAAACA 4022  
 RESULT 43  
 AAC69153/c  
 ID AAC69153 standard; DNA; 18 BP.  
 AC AAC69153;  
 XX  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 phosphorothioate antisense oligonucleotide AN-7.  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal;  
 KW phosphorothioate antisense oligonucleotide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200055318-A2.  
 XX  
 PD 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-IB00532.  
 XX  
 XX 15-MAR-1999; 99US-0124702.  
 PR 08-JUN-1999; 99US-0138048.  
 PR 17-JUN-1999; 99US-0139600.  
 PR 01-SEP-1999; 99US-0151977.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Wilson AR, Pimstone SN;  
 XX  
 XX WPI; 2000-587528/55.  
 DR  
 XX  
 PT New ABC1 polypeptide is useful for treating diseases associated with  
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 PT disease and cancer.  
 XX  
 XX Examples; Page 39; 229pp; English.  
 XX  
 CC The invention relates to the human ABC1 cholesterol transporter protein  
 CC (B38082) and to nucleic acid sequences (c69120) which encode it. ABC1 is  
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
 CC proteins, and plays a crucial role in cholesterol transport, particularly  
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is

CC located on chromosome 9q31, and mutations in this gene are associated  
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary restenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds.  
 CC It further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 CC or prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary restenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated  
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
 CC present sequence represents a human ABC-1 cDNA-specific phosphorothioate  
 CC antisense oligonucleotide used in the exemplifications of the invention.  
 XX  
 SQ Sequence 18 BP; 3 A; 8 C; 3 G; 4 T; 0 other;  
 Query Match 11.3%; Score 18; DB 21; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 79 gctggctgagggaacatg 96  
 Db 18 GCTGGCTGAGGGAACATG 1  
 RESULT 44  
 ABL08833/c  
 ID ABL08833 standard; cDNA; 6420 BP.  
 XX  
 AC ABL08833;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 20981.  
 DE  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 KW  
 XX Drosophila melanogaster.  
 OS  
 XX W0200171042-A2.  
 PN  
 XX 27-SEP-2001.  
 PD  
 XX  
 XX 23-MAR-2001; 2001WO-US09231.  
 PF  
 XX 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 PR  
 XX (PEKE ) PE CORP NY.  
 PA  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 PI  
 XX WPI; 2001-656860/75.  
 DR P-PSDB; ABB64730.  
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -

XX Claim 1; SEQ ID NO 20981; 2lpp + Sequence Listing; English.

PS The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 6420 BP; 1886 A; 1829 C; 1603 G; 1102 T; 0 other;

Query Match 11.3%; Score 18; DB 23; Length 6420;

Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 agctgaggttgcctgt 127

DB 4817 AGCTGAGGTGCTGCTGT 4800

RESULT 45

ABL08832/C

ID ABL08832 standard; cDNA; 11580 BP.

XX ABL08832;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 20978.

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR P-PSDB; ABB64729.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -

PS Claim 1; SEQ ID NO 20978; 2lpp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 11580 BP; 3621 A; 2752 C; 2467 G; 2740 T; 0 other;

Query Match 11.3%; Score 18; DB 23; Length 11580;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 agctgaggttgcctgt 127

DB 6963 AGCTGAGGTGCTGCTGT 6946

Search completed: September 20, 2002, 06:08:29

Job time: 10393 sec





```
RESULT 2
US-08-975-316-9
; Sequence 9, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-9

Query Match 11.9%; Score 19; DB 2; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctgggctgtgctgctgag 88
Db 261 GCTGGCGGTGCTGGCTGAG 279

RESULT 3
US-09-211-710-9
; Sequence 9, Application US/09211710A
; Patent No. 6204434
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N.
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Grierson, Alastair
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C3
; CURRENT APPLICATION NUMBER: US/09/211,710A
; CURRENT FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
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```
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-211-710-9

Query Match 11.9%; Score 19; DB 4; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctgggctgtgctgctgag 88
Db 261 gctgggctgtgctgctgag 279

RESULT 4
US-08-975-316-45
; Sequence 45, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-45

Query Match 11.9%; Score 19; DB 2; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 gctgggctgtgctgctgag 88
Db 261 GCTGGCGGTGCTGGCTGAG 279

RESULT 5
US-08-519-777-63/c
; Sequence 63, Application US/08519777
```

; Patent No. 5739307  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/519,777  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-519-777-63

Query Match 10.1%; Score 16; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
Db 36 ggcgcgtgccttcag 21

RESULT 6  
US-08-742-035-63/c  
; Sequence 63, Application US/08/42035  
; Patent No. 5747655  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/742,035  
; FILING DATE: 01-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-742-035-63

Query Match 10.1%; Score 16; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
Db 36 ggcgcgtgccttcag 21

RESULT 7  
US-08-777-019-63/c  
; Sequence 63, Application US/08/777019  
; Patent No. 5817622  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,019  
; FILING DATE: 30-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-777-019-63

Query Match 10.1%; Score 16; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
DB 36 ggcgcgtgccttcag 21

## RESULT 8

US-08-777-143-63/c  
; Sequence 63, Application US/08777143  
; Patent No. 5843914  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,143  
; FILING DATE: 30-DEC-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-777-143-63

Query Match 10.1%; Score 16; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 ggcgcgtgccttcag 53  
|||||  
Db 36 ggcgcgtgccttcag 21

## RESULT 9

US-08-775-414-63/c  
; Sequence 63, Application US/08775414  
; Patent No. 6090778  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/775,414  
; FILING DATE: 31-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965805  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-775-414-63

Query Match 10.1%; Score 16; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
DB 36 ggcgcgtgccttcag 21

## RESULT 10

US-08-931-858E-63/c  
; Sequence 63, Application US/08931858E  
; Patent No. 6222022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; APPLICANT: KLEIN, ROBERT  
; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:

;  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931.858E  
; FILING DATE:  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971486  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-931-858E-63

Query Match 10.1%; Score 16; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 38 ggcgcgtgccttcag 53  
|||||  
Db 36 GCGCGCTGCCTTCAG 21

RESULT 11  
US-08-981-739-63/c  
; Sequence 63, Application US/08981739  
; Patent No. 6232449  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; MILBRANDT, JEFFREY D.  
; KOTZBAUER, PAUL T.  
; LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981.739  
; FILING DATE: 31-Aug-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/03461  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976163  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:  
US-08-981-739-63

Query Match 10.1%; Score 16; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 38 ggcgcgtgccttcag 53  
|||||  
Db 36 GCGCGCTGCCTTCAG 21

RESULT 12  
US-08-519-777-18/c  
; Sequence 18, Application US/08519777  
; Patent No. 5739307  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/519,777  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 57 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-519-777-18

Query Match 10.1%; Score 16; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 38 ggcgcgtgccttcag 53  
|||||  
Db 24 GCGCGCTGCCTTCAG 9

RESULT 13  
US-08-742-035-18/c

; Sequence 18, Application US/08742035  
; Patent No. 5747655  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/742,035  
; FILING DATE: 01-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 57 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; US-08-742-035-18

Query Match 10.1%; Score 16; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
Db 24 GGCGCTGCCTCCAG 9

RESULT 14  
US-08-777-019-18/c  
; Sequence 18, Application US/08777019  
; Patent No. 5817622  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,019  
; FILING DATE: 30-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 57 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; US-08-777-019-18

Query Match 10.1%; Score 16; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
Db 24 GGCGCTGCCTCCAG 9

RESULT 15  
US-08-777-143-18/c  
; Sequence 18, Application us/08777143  
; Patent No. 5843914  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,143  
; FILING DATE: 30-DEC-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 57 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-777-143-18

Query Match 10.1%; Score 16; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
DB 24 GGCCTGCTTCCAG 9

RESULT 16  
US-08-775-414-18/c  
Sequence 18, Application US/08775414  
Patent No. 6090778  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: NEUTURIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 31-DEC-1996  
APPLICATION NUMBER: US/08/775,414  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965805  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 57 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-775-414-18

Query Match 10.1%; Score 16; DB 3; Length 57;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
DB 24 GGCCTGCTTCCAG 9

RESULT 17  
US-08-931-858E-18/c  
Sequence 18, Application US/08931858E  
Patent No. 6222022  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 57 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-931-858E-18

Query Match 10.1%; Score 16; DB 4; Length 57;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||  
DB 24 GGCCTGCTTCCAG 9

RESULT 18  
US-08-981-739-18/c  
Sequence 18, Application US/08981739  
Patent No. 6232449  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/981,739
; FILING DATE: 31-Aug-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-981-739-18

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Query Match 10.1%; Score 16; DB 4; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 ggccgctgccttcacg 53  
 |||||||||||||  
 Db 24 GGCGCTGCCTTCCAG 9

```

RESULT 19
; Sequence 29, Application US/08519777
; Patent No. 5739307
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,777
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092

```

```

; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-519-777-29

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Query Match 10.1%; Score 16; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 ggccgctgccttcacg 53  
 |||||||||||||  
 Db 24 GGCGCTGCCTTCCAG 9

```

RESULT 20
; Sequence 29, Application US/08742035
; Patent No. 5747655
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,035
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-742-035-29

```

Query Match 10.1%; Score 16; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 ggccgctgccttcacg 53  
 |||||||||||||  
 Db 24 GGCGCTGCCTTCCAG 9

RESULT 21  
US-08-777-019-29/c  
; Sequence 29, Application US/08777019  
; Patent No. 5817622  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,019  
; FILING DATE: 30-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-777-019-29

Query Match 10.1%; Score 16; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 ggcgcgtgccttcag 53  
DB 24 GCGCGCTGCTTCCAG 9

RESULT 22  
US-08-777-143-29/c  
; Sequence 29, Application US/08777143  
; Patent No. 5843914  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS

; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,143  
; FILING DATE: 30-DEC-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-777-143-29

Query Match 10.1%; Score 16; DB 2; Length 169;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 ggcgcgtgccttcag 53  
DB 24 GCGCGCTGCTTCCAG 9

RESULT 23  
US-08-775-414-29/c  
; Sequence 29, Application US/08775414  
; Patent No. 6090778  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/775,414  
; FILING DATE: 31-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965805  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 169 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-775-414-29

Query Match 10.1%; Score 16; DB 3; Length 169;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||

Db 24 ggcgcgtgccttcag 9

## RESULT 24

US-08-931-858E-29/C  
; Sequence 29, Application US/08931858E  
; Patent No. 6222022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M  
; APPLICANT: MILBRANDT, JEFFREY D  
; APPLICANT: KOTZBAUER, PAUL T  
; APPLICANT: LAMPE, PATRICIA A  
; APPLICANT: KLEIN, ROBERT  
; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,858E  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971486  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-931-858E-29

Query Match 10.1%; Score 16; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||

Db 24 ggcgcgtgccttcag 9

## RESULT 25

US-08-981-739-29/c  
; Sequence 29, Application US/08981739  
; Patent No. 6232449  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; MILBRANDT, JEFFREY D.  
; KOTZBAUER, PAUL T.  
; LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,739  
; FILING DATE: 31-Aug-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/03461  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976163  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-08-981-739-29

Query Match 10.1%; Score 16; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
|||||

Db 24 ggcgcgtgccttcag 9

## RESULT 26

US-08-519-777-26/c  
; Sequence 26, Application US/08519777  
; Patent No. 5739307  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/519,777  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 953095  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-519-777-26

Query Match 10.1%; Score 16; DB 1; Length 285;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgcctccag 53  
DB 24 GCGCGCTGCCTCCAG 9

RESULT 27  
US-08-742-035-26/c  
Sequence 26, Application US/08742035  
Patent No. 5747655  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/742,035  
FILING DATE: 01-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/519,777  
FILING DATE: 28-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 953095  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-742-035-26

Query Match 10.1%; Score 16; DB 1; Length 285;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgcctccag 53  
DB 24 GCGCGCTGCCTCCAG 9

RESULT 28  
US-08-777-019-26/c  
Sequence 26, Application US/08777019  
Patent No. 5817622  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,019  
FILING DATE: 30-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/519,777  
FILING DATE: 28-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 953095  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-777-019-26

Query Match 10.1%; Score 16; DB 1; Length 285;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
| | | | | | | | | |  
Db 24 GGCGCTGCCTTCAG 9

RESULT 29  
US-08-777-143-26/c  
; Sequence 26, Application US/08777143  
; Patent No. 5843914  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,143  
; FILING DATE: 30-DEC-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/519,777  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 285 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-777-143-26

Query Match 10.1%; Score 16; DB 2; Length 285;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
| | | | | | | | | |  
Db 24 GGCGCTGCCTTCAG 9

RESULT 30  
US-08-775-414-26/c  
; Sequence 26, Application US/08775414  
; Patent No. 6090778  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 90

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/775,414  
; FILING DATE: 31-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965805  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 285 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-775-414-26

Query Match 10.1%; Score 16; DB 3; Length 285;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcag 53  
| | | | | | | | | |  
Db 24 GGCGCTGCCTTCAG 9

RESULT 31  
US-08-931-858E-26/c  
; Sequence 26, Application US/08931858E  
; Patent No. 6222022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; APPLICANT: KLEIN, ROBERT  
; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,858E  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-931-858E-26

Query Match 10.1%; Score 16; DB 4; Length 285;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 ggcgcgtgccttcag 53  
Db 24 ggcgcgtgccttcag 9

RESULT 32  
US-08-981-739-26/c  
Sequence 26, Application US/08981739  
Patent No. 6232449  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-08-981-739-26

Query Match 10.1%; Score 16; DB 4; Length 285;

Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 ggcgcgtgccttcag 53  
Db 24 ggcgcgtgccttcag 9

RESULT 33  
US-08-519-777-12/c  
Sequence 12, Application US/08519777  
Patent No. 5739307  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
LAMPE, PATRICIA A.  
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/519,777  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 953095  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 585 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-519-777-12

Query Match 10.1%; Score 16; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 ggcgcgtgccttcag 53  
Db 24 ggcgcgtgccttcag 9

RESULT 34  
US-08-742-035-12/c  
Sequence 12, Application US/08742035  
Patent No. 5747655  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
LAMPE, PATRICIA A.  
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,035
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-742-035-12

Query Match 10.1%; Score 16; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcacg 53
Db 24 GCGCGCTGCCTTCCAG 9

RESULT 35
US-08-777-019-12/c
; Sequence 12, Application US/08777019
; Patent No. 5817622
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,019
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777

```

```

; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-777-019-12

Query Match 10.1%; Score 16; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcacg 53
Db 24 GCGCGCTGCCTTCCAG 9

RESULT 36
US-08-777-143-12/c
; Sequence 12, Application US/08777143
; Patent No. 5843914
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,143
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-777-143-12

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Query Match 10.1%; Score 16; DB 2; Length 585;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgcctccag 53  
|||||  
DB 24 GGCGCTGCCTCCAG 9

RESULT 37  
US-08-775-414-12/c  
; Sequence 12, Application US/08775414  
; Patent No. 6090778  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/775.414  
; FILING DATE: 31-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965805  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 585 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-775-414-12

Query Match 10.1%; Score 16; DB 3; Length 585;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgcctccag 53  
|||||  
DB 24 GGCGCTGCCTCCAG 9

RESULT 38  
US-08-931-858E-12/c  
; Sequence 12, Application US/08931858E  
; Patent No. 6222022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; APPLICANT: KLEIN, ROBERT

; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,858E  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971486  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092

; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 585 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-931-858E-12

Query Match 10.1%; Score 16; DB 4; Length 585;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgcctccag 53  
|||||  
DB 24 GGCGCTGCCTCCAG 9

RESULT 39  
US-08-981-739-12/c  
; Sequence 12, Application US/08981739  
; Patent No. 6232449  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; MILBRANDT, JEFFREY D.  
; KOTZBAUER, PAUL T.  
; LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,739  
; FILING DATE: 31-Aug-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/03461  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 585 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-08-981-739-12

Query Match 10.1%; Score 16; DB 4; Length 585;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcacg 53  
|||||  
DB 24 GCGCGCTGCCTTCAG 9

RESULT 40  
US-08-931-858E-49/c  
; Sequence 49, Application US/08931858E  
; Patent No. 622022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M  
; APPLICANT: MILBRANDT, JEFFREY D  
; APPLICANT: KOTZBAUER, PAUL T  
; APPLICANT: LAMPE, PATRICIA A  
; APPLICANT: KLEIN, ROBERT  
; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,858E  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971486  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1023 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-931-858E-49

Query Match 10.1%; Score 16; DB 4; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ggcgcgtgccttcacg 53  
|||||  
DB 372 GCGCGCTGCCTTCAG 357

RESULT 41  
US-08-697-954-3/c  
; Sequence 3, Application US/08697954  
; Patent No. 6284535  
; GENERAL INFORMATION:  
; APPLICANT: Role, Lorna W.  
; TITLE OF INVENTION: SPLICE VARIANTS OF THE HERGULIN GENE, PARIA, AND  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/697,954  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 46839-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0526  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1351 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-697-954-3

Query Match 10.1%; Score 16; DB 4; Length 1351;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 gaacctcacttcaga 147  
|||||  
DB 552 GAACCTCACTTCAGA 537

RESULT 42  
US-08-428-926-1/c  
; Sequence 1, Application US/08428926  
; Patent No. 5667780  
; GENERAL INFORMATION:  
; APPLICANT: Ho, Wei-Hsien  
; APPLICANT: Osherooff, Phyllis L.  
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,926  
FILING DATE: 25-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/339517  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 853D4  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1872 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-428-926-1

Query Match 10.1%; Score 16; DB 1; Length 1872;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 gaacctcactttcaga 147  
|||||  
Db 966 GAACCTCACTTTTCAGA 951

RESULT 43  
US-08-435-434-4/c  
Sequence 4, Application US/08435434  
Patent No. 5714385  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,434  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-2  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1872 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-434-4

Query Match 10.1%; Score 16; DB 1; Length 1872;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 gaacctcactttcaga 147  
|||||  
Db 966 GAACCTCACTTTTCAGA 951

RESULT 44  
US-08-435-436-4/c  
Sequence 4, Application US/08435436  
Patent No. 5721139  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,436  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-3  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1872 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-436-4

Query Match 10.1%; Score 16; DB 1; Length 1872;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: September 20, 2002, 06:15:35  
Job time: 11154 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 04:07:29 ; Search time 3900.56 Seconds  
(without alignments)  
550.181 Million cell updates/sec

Title: US-09-846-456-5  
Perfect score: 159  
Sequence: 1 ttaatgaccgacccagcg.....ctttcagaagaagacaaaca 159

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- EST:\*
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estin:\*
  - 4: em\_estnu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_hic:\*
  - 9: gb\_est1:\*
  - 10: gb\_est2:\*
  - 11: gb\_hic:\*
  - 12: gb\_gss:\*
  - 13: em\_gss\_hum:\*
  - 14: em\_gss\_inv:\*
  - 15: em\_gss\_pln:\*
  - 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	32.1	736	9	AU135588
2	39	24.5	535	10	BG384217
3	24	15.1	292	10	Z44377 HSC12E081 n
4	20	12.6	661	10	BI391126
5	19	11.9	216	10	BF756949
6	19	11.9	454	12	AQ369174
7	19	11.9	470	9	AI353952
8	19	11.9	493	12	AQ709464
9	19	11.9	618	9	AA495487
10	19	11.9	643	9	AI497295
11	19	11.9	705	10	BI160520
12	19	11.9	730	9	AW116004
13	18	11.3	231	10	BF898523
14	18	11.3	275	12	BH402163
15	18	11.3	299	9	AA098714
16	18	11.3	303	10	BF903506
17	18	11.3	375	12	BH127062

18	18	11.3	397	10	BF911983	BF911983 IL2-UT007
19	18	11.3	529	12	BH396354	BH396354 AG-ND-161
20	18	11.3	532	12	AQ776697	AQ776697 HS-2148.B
21	18	11.3	532	12	AQ779444	AQ779444 HS-2001.A
22	18	11.3	554	12	AZ236353	AZ236353 RPC1-23-7
23	18	11.3	558	12	AZ510640	AZ510640 IM0355G15
24	18	11.3	566	12	AZ510673	AZ510673 IM0355M15
25	18	11.3	599	9	AA720413	AA720413 ET2347 Tr
26	18	11.3	631	9	AL652524	AL652524 AL652524
27	18	11.3	645	9	BB614720	BB614720 BB614720
28	18	11.3	645	10	BI996688	BI996688 103104180
29	18	11.3	647	12	CNS03C31	AL237303 Tetraodon
30	18	11.3	654	10	BG308188	BG308188 fm58c10.Y
31	18	11.3	672	12	BH375609	BH375609 AG-ND-165
32	18	11.3	683	9	AW565995	AW565995 LGL-354.G
33	18	11.3	689	9	AL648437	AL648437 AL648437
34	18	11.3	693	9	AV868908	AV868908 AV868908
35	18	11.3	712	10	BI254723	BI254723 602978612
36	18	11.3	796	10	BI906710	BI906710 603064430
37	18	11.3	809	12	BH181298	BH181298 018_I-20-
38	18	11.3	809	12	CNS07MYE	AL618248 T3 end of
39	18	11.3	855	12	BH475331	BH475331 BOGYG96TF
40	18	11.3	887	10	BI464093	BI464093 603202870
41	18	11.3	961	12	CNS02ELU	AL193899 Tetraodon
42	17	10.7	131	9	AW670238	AW670238 114155 MA
43	17	10.7	202	10	BF562309	BF562309 UT-R-BS0-
44	17	10.7	218	9	BB183552	BB183552 BB183552
45	17	10.7	249	9	AV061772	AV061772 AV061772

ALIGNMENTS

RESULT 1  
AU135588  
LOCUS AU135588 PLACE1 Homo sapiens cdna clone PLACE1002437 5', mRNA  
DEFINITION AU135588.1 GI:10996127  
ACCESSION AU135588  
VERSION AU135588.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 736)  
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.  
TITLE HRI human cdna project  
JOURNAL Unpublished (2000)  
COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomics@hri.co.jp  
HRI human cdna project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cdna library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="PLACE1002437"  
/clone\_lib="PLACE1"  
/tissue\_type="placenta"  
/note="Vector: pME18SFL3"

BASE COUNT 163 a 199 g 199 g 170 t 5 others  
ORIGIN

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Query Match      32.1%; Score 51; DB 9; Length 736;
Best Local Similarity 100.0%; Pred. No. 6e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 cagctgaggctgtctgtggaagaacctcacttcagaagaagaaca 159
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Db 329 CAGCTGAGGTGCTGCTGTGGAAGACCTCACTTTCAGAAGAGACAACA 379

RESULT 2
LOCUS      BG384217          535 bp mRNA linear EST 12-MAR-2001
DEFINITION 303216 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  BG384217
VERSION     BG384217.1 GI:13308689
KEYWORDS   EST.
SOURCE     pig.
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 535)
AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keeler,J.W.
TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
JOURNAL   Unpublished (2000)
COMMENT   Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@mail.marc.usda.gov
            Single pass sequencing. Bases called and alt.trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACGATGACCAT
BACKWARD: GTTTCGCCAGTCAGCAGC
Plate: 90 row: G column: 13
Seq primer: ATTTAGTGACACTATAG.
            Location/Qualifiers
            1..535
               /organism="Sus scrofa"
               /db_xref="taxon:9823"
               /clone_lib="MARC 1P1G"
               /tissue_type="pooled"
               /lab_host="DH10B"
               /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
               Library made from pooled tissue from day 11, 13, 15, 20,
               and 30 embryos."
BASE COUNT      121 a 159 c 136 g 119 t
ORIGIN

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Query Match      24.5%; Score 39; DB 10; Length 535;
Best Local Similarity 100.0%; Pred. No. 9.9e-10;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 ctgctgtggaagaacctcacttcagaagaagaaca 159
|||||.....|.....|.....|.....|.....|.....|.....|
Db 311 CTGCTGTGGAAGACCTCACTTTCAGAAGAGACAACA 349

RESULT 3
LOCUS      Z44377          292 bp mRNA linear EST 14-NOV-1994
DEFINITION  HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone
ACCESSION  Z44377
VERSION     Z44377.1 GI:573506
KEYWORDS   C-12b08, mRNA sequence.

SOURCE     chicken.
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 661)
            Porter,T.E. and Cogburn,L.A.
            ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
            Library USDA/IFAFS Animal Genome Project

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 292)
AUTHORS   Aufray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
            M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
            Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE   95277534
COMMENT   Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-12b08
            Seq primer: (-21)M13_universal.
            Location/Qualifiers
            1..292
               /organism="Homo sapiens"
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               /tissue_type="total brain"
               /dev_stage="3 months old"
               /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
               Site_2: NotI; sex=Female; dev_stage=3 months old;
               isolate=muscular atrophy patient; tissue_type=total brain
               isolated=muscular atrophy patient; primed and directionally
               cloned 5' -> 3' into the HindIII -> NotI sites of the
               lafmid BA vector. Clone library from B.Souares, Psychiatry
               Dept. Columbia University, USA. Normalization_method:
               Bento Soares, P.N.A.S in press"
BASE COUNT      50 a 87 c 96 g 56 t 3 others
ORIGIN

```

JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Larry A. Cogburn  
University of Delaware  
Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1335  
Fax: 302-831-2822  
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES  
source

1. .661  
Location/Qualifiers  
/organism="Gallus gallus"  
/strain="Commercial broiler chicken"  
/db\_xref="taxon:9031"  
/clone="pgpln.pk003.g18"  
/clone.lib="Normalized Chicken  
Pituitary/Hypothalamus/Pineal Library"  
/sex="Male and female"  
/tissue\_type="Pituitary Gland/Hypothalamus/Pineal Gland"  
/dev\_stage="Embryonic (d12,d14,d19); post-hatch (w1,w3,w5,w7,w9)"  
/lab\_host="E. Coli EMDH10B"  
/note="Vector: pCMVSPORT6; Library made from equivalent  
pools of total RNA isolated from each tissue at different  
ages. Single pass sequencing from 5'-end"  
BASE COUNT 155 a 164 c 225 g 117 t  
ORIGIN

Query Match  
Best Local Similarity

12.6%; Score 20; DB 10; Length 661;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

69 cgcctggcgtgctgctgaag 88

Db

63 CGCTGGCGCTGCTGCTGAG 82

RESULT 5  
BF756949/c

LOCUS BF756949 216 bp mRNA linear EST 12-JAN-2001  
DEFINITION CM1-CT0424-011100-522-e09 CT0424 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF756949  
VERSION BF756949.1 GI:12104849  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 216)

REFERENCE  
AUTHORS

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL  
MEDLINE

20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

## COMMENT

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM1&t2=CM1-CT0424-  
011100-522-e09&t3=2000-11-01&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 216.  
Location/Qualifiers

## FEATURES

Query Match 11.9%; Score 19; DB 12; Length 454;  
Best Local Similarity 100.0%; Pred. No. 26;

## source

1. .216  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone.lib="CT0424"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 48 a 39 c 49 g 80 t  
ORIGIN

## Query Match

11.9%; Score 19; DB 10; Length 216;

## Best Local Similarity

100.0%; Pred. No. 21;

## Matches

19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

141 ttccagaagaagacaaaca 159

Db

160 TTTCAGAAGAAGACAAACA 142

## RESULT 6

AQ369174

LOCUS AQ369174 454 bp DNA linear GSS 06-MAR-1999

DEFINITION HS\_5032\_A2\_F04\_SP6E RPC111 Human Male BAC Library Homo sapiens

genomic clone Plate=608 Col=8 Row=K, DNA sequence.

ACCESSION AQ369174

VERSION AQ369174.1 GI:4338653

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 454)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

JOURNAL 9380589

MEDLINE

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 608 row: K column: 8

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 454.

Location/Qualifiers

1. .454

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="plate=608 Col=8 Row=K"

/clone.lib="RPC111 Human Male BAC Library"

/sex="Male"

/cell\_type="Lymphocytes"

/note="vector: pBACE3.6; RPC111 Human Male BAC Library"

BASE COUNT 144 a 82 c 90 g 136 t

ORIGIN

2 others

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 cagctggcgtgctgct 85

Db 285 CACGCTGGCGTGTGCT 303

# RESULT 7

AI353952/c

LOCUS

DEFINITION

zehl1204.seq\_F Zebrafish Embryonic Heart cDNA Library Danio rerio

CDNA 5', mRNA sequence.

ACCESSION

AI353952

VERSION

AI353952.1 GI:4094105

KEYWORDS

EST.

SOURCE

zebrafish.

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

1 (bases 1 to 470)

REFERENCE

1 (bases 1 to 470)

AUTHORS

Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and Liew

C.C.

TITLE

Identification and Characterization of Expressed Sequence Tags from

an Embryonic Zebrafish Heart cDNA Library

JOURNAL

Unpublished (1999)

COMMENT

Contact: Liew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750995

Email: cliew@rics.bwh.harvard.edu

PCR Primers

FORWARD: 5' GCCAAGCTCGAATTAACCTCACTAAAGGG 3'

BACKWARD: 5' CCAGTGAAATGTATACGACTCATATAGGGG 3'

Seq primer: 5' GAATTAACCTCACTAAAGGG 3'

Location/Qualifiers

1..470

/organism="Danio rerio"

/db\_xref="taxon:7955"

/clone\_lib="zebrafish Embryonic Heart cDNA Library"

/lab\_stage="embryonic day 3 post-fertilization"

/lab\_host="E.coli XL1-Blue MRF"

/note="Organ: heart; Vector: Lambda ZAP Express; Site:1:

EcoRI; Site:2: XhoI; mRNA was purified from embryonic

zebrafish hearts (3 day post-fertilization). cDNA was

synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI

adaptors were ligated, followed by digestion with XhoI,

for directional cloning into pre-digested lambda ZAP

Express vector."

BASE COUNT

123 a 112 c 130 g 105 t

ORIGIN

Query Match

Best Local Similarity 11.9%; Score 19; DB 9; Length 470;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 tggcctcagctgaggttgc 121

Db 395 TGGCCTCAGCTGAGGTGCT 377

# ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 493)

AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

JOURNAL

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

MEDLINE

99380589

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1035 row: K column: 8

Seq primer: T7

Class: BAC ends

High quality sequence stop: 493.

Location/Qualifiers

1..493

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="Plate=1035 Col=8 Row=K"

/clone\_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACE3.6; Site:1: EcoRI; Site:2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACE3.6 vector at EcoRI sites"

BASE COUNT

171 a 94 c 69 g 152 t 7 others

ORIGIN

Query Match

Best Local Similarity 11.9%; Score 19; DB 12; Length 493;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 139 actttcagaagaagacaaa 157

Db 478 ACTTTTCAGAAGAAGACAAA 460

RESULT 9

AA495487/c

LOCUS

DEFINITION

fa09h12.r1 zebrafish ICRFzfls Danio rerio cDNA clone 1108 5'

similar to gb:J04973 UBIQUINOL-CYTOCHROME C REDUCTASE CORE PROTEIN

2 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION

AA495487

VERSION

AA495487.1 GI:2224979

KEYWORDS

EST.

SOURCE

zebrafish.

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

1 (bases 1 to 618)

REFERENCE

1 (bases 1 to 618)

AUTHORS

Clark,M., Lehrach,H., Appel,B., Eisen,J., Johnson,S., Marra,M.,

Eddy,S., Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,

Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Martin,J., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie

T., Waterston,R. and Wilson,R.

TITLE  
JOURNAL  
COMMENT

WashU Zebrafish EST Project  
Unpublished (1997)  
Contact: Steve Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.  
WashU Zebrafish EST Project 1998  
Unpublished (1998)  
Contact: Stephen L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Steve Johnson lab internal ID - P3\_96 NOTE - For this library, the CLONE id field represents a position identifier on the original cDNA library preparation plate. cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare Genetik, Berlin Tel +49 30 84 13 1235  
Seq primer: T7 ET from Amersham  
High quality sequence stop: 427.

FEATURES  
Source

1. 618  
Location/Qualifiers  
/organism="Danio rerio"  
/db\_xref="taxon:7955"  
/clone="1108"  
/clone\_lib="Zebrafish ICRZFzfls"  
/sex="mixed"  
/tissue\_type="pooled 26-somite embryos"  
/lab\_host="X11-blue MRF"  
/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'PGACTAGTCTAGATCGAGCGCGCCGCTTTT3'], on mRNA from pooled 26 somite zebrafish embryos; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin) and was not biochemically normalised. 70,000 clones from this library were arrayed on high density filters and subsequently screened by oligonucleotide hybridization fingerprinting to identify unique or minimally redundant clones for more intensive analysis."

BASE COUNT 150 a 161 c 168 g 139 t  
ORIGIN

Query Match 11.9%; Score 19; DB 9; Length 618;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 tggcctcagctgaggttgc 121  
|||||  
Db 299 TGGCCTCAGCTGAGGTTCG 281

RESULT 10  
AI497295/c  
LOCUS  
DEFINITION  
fb63g04.v1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3716598 5', similar to SW:UCR2\_HUMAN P22695  
UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR  
; mRNA sequence.  
AI497295  
AI497295.1 GI:4398298  
EST  
KEYWORDS  
SOURCE  
ORGANISM  
zebrafish.

Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 643)  
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,

FEATURES  
Source

1. 643  
Location/Qualifiers  
/organism="Danio rerio"  
/db\_xref="taxon:7955"  
/clone="IMAGE:3716598"  
/clone\_lib="zebrafish WashU MPIMG EST"  
/sex="mixed"  
/tissue\_type="26 somite embryos, adult livers, shield stage embryos"  
/lab\_host="X11-blue MRF"  
/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'PGACTAGTCTAGATCGAGCGCGCCGCTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

BASE COUNT 164 a 158 c 170 g 150 t  
ORIGIN

Query Match 11.9%; Score 19; DB 9; Length 643;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 tggcctcagctgaggttgc 121  
|||||  
Db 395 TGGCCTCAGCTGAGGTTCG 377

RESULT 11  
BI160520  
LOCUS  
DEFINITION  
602864591F1 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:5018519 5', mRNA sequence.  
BI160520  
ACCESSION  
BI160520.1 GI:14620521

BT160520 705 bp mRNA linear EST 05-JUL-2001

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 705)  
JOURNAL NIH-MGC <http://mgc.nci.nih.gov/>.  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@email.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI832 row: f column: 24  
High quality sequence stop: 591.  
Location/Qualifiers  
1..705  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5018519"  
/clone\_lib="NIH\_MGC\_42"  
/tissue\_type="epithelioid carcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: pancreas; Vector: pORF7; Site:1: XhoI;  
Site:2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: This is a NIH-MGC Library. |"  
BASE COUNT 152 a 209 c 224 g 120 t  
ORIGIN

Query Match 11.9%; Score 19; DB 10; Length 705;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 agctgaggttgctgctgtg 128  
|||||  
Db 682 AGCTGAGGTTGCTGCTGTG 700

RESULT 12  
LOCUS AW116004  
DEFINITION f106a11.x1 Sugano Kawakami zebrafish DRA Danio rerio CDNA clone  
2600348 3' similar to SW:UCR2\_BOVIN P23004 UBIOUINOL-CYTOCHROME C  
REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR ;, mRNA sequence.  
ACCESSION AW116004  
VERSION AW116004.1 GI:6082342  
KEYWORDS EST.  
SOURCE zebrafish.  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes  
; Cyprinidae; Danio.  
1 (bases 1 to 730)  
Sugano, S.; Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S.,  
Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T.,  
Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Ritter  
E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU Zebrafish EST Project 1999  
Unpublished (1999)  
Contact: S.L. Johnson  
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA  
Sequencing by: Washington University Genome Sequencing Center  
zebrafish identity (p-value greater than 1e-99) found to:  
[gil22249791gb/AA495487/AA495487](http://gil22249791gb/AA495487/AA495487.fa09h12.r1) fa09h12.r1 zebrafish ICRPzfls Danio  
rerio CDNA  
Seq primer: T7 ET from Amersham  
High quality sequence stop: 450.  
Location/Qualifiers  
1..730  
/organism="Danio rerio"  
/strain="AB"  
/db\_xref="taxon:7955"  
/clone\_lib="Sugano Kawakami zebrafish DRA"  
/clone="2600348"  
/sex="mixed (one male and one female, including  
unfertilized eggs)"  
/dev\_stage="adult"  
/lab\_host="DH10B (phage resistant)"  
/note="Vector: pME18S-FL3; Site\_1: DraIII (CACGTGTGG);  
Site\_2: DraIII (CACCATGTG); 1st strand CDNA was primed  
with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTT];  
double-stranded cDNA was ligated to a DraIII adaptor  
[TGTGGCTACTGG], digested and cloned into distinct DraIII  
sites of the pME18S-FL3 vector (5' site CACGTGTGG, 3' site  
CACCATGTG). XhoI should be used to isolate the CDNA  
insert. Size selection was performed to exclude fragments  
<1.5kb. Library constructed by Dr. Sumio Sugano  
(University of Tokyo Institute of Medical Science) and  
kindly donated by Dr. Koichi Kawakami. Custom primers for  
sequencing: 5' end primer CTTCGTGCTAAAGCTGCG and 3' end  
primer CGACCTGCAGCTCAGGACACA."  
BASE COUNT 195 a 167 c 168 g 198 t  
ORIGIN

Query Match 11.9%; Score 19; DB 9; Length 730;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 tggcctcagctgaggttgc 121  
|||||  
Db 673 TGGCCTCAGCTGAGGTTCG 691

RESULT 13  
LOCUS BF898523  
DEFINITION CMI-MT0188-291100-611-g02 MT0188 Homo sapiens CDNA, mRNA sequence.  
ACCESSION BF898523  
VERSION BF898523.1 GI:12289982  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 231)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Fax: +55-11-2704922

Fax: +55-11-2707001

Email: asmpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1st2-CM1-WT0188-291100-611-d02st3-2000-11-29st4-1>)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 231.

Location/Qualifiers

1. 231

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="MT0188"

/dev\_stage="Adult"

/note="Organ: marrow; Vector: puc18; Site:1; SmaI; Site:2; SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

39 a 48 c 82 g 62 t

BASE COUNT  
ORIGIN

Query Match 11.3%; Score 18; DB 10; Length 231;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ctggctgagggaacatgg 97

|||||

Db 182 CTGGCTGAGGACATGG 199

RESULT 14  
BH402163/c

LOCUS

DEFINITION BH402163 AG-ND-102E12.TF ND-TAM Anopheles gambiae genomic clone AG-ND-102E12

, DNA sequence.

ACCESSION BH402163

VERSION BH402163.1

KEYWORDS GSS.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea

; Anopheles.

REFERENCE 1 (bases 1 to 275)

Shetty J., Malek J., Koo H., Collins F., Gardner M. and Loftus B.J.

Direct Submission of BAC-end sequences from Anopheles gambiae

Unpublished (2001)

Other\_GSSs: AG-ND-102E12.TF

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b.loftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.

Seq primer: M13 For

Class: BAC ends  
Location/Qualifiers  
1. 275  
/organism="Anopheles gambiae"  
/strain="PEST"  
/db\_xref="taxon:7165"  
/clone="AG-ND-102E12"  
/clone\_lib="ND-TAM"  
/note="Vector: pECBAC1; Site:1: HindIII"  
73 a 47 c 73 g 82 t

BASE COUNT  
ORIGIN

Query Match 11.3%; Score 18; DB 12; Length 275;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 acttcagaagaagacaa 156  
|||||

Db 207 ACTTTCAGAGAGACAA 190  
|||||

RESULT 15  
AA098714/c

LOCUS

DEFINITION T4026 MVAT4 bloodstream form of serodeme WRATat1.1 Trypanosoma

ACCESSION AA098714

VERSION AA098714.1

KEYWORDS EST.

SOURCE Trypanosoma brucei rhodesiense.

ORGANISM Trypanosoma brucei rhodesiense  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 299)  
Djikeng A., Donelson J.E. and Majiwa P.A.O.  
Generation of expressed sequence tags as physical landmarks in the genome of Trypanosoma brucei  
Unpublished (1996)  
Contact: Majiwa PAO  
Molecular Biology Unit  
International Livestock Research Institute  
P.O. Box 30709, Nairobi, Kenya  
Tel: 254-2 630743  
Fax: 254-2 631499  
Email: p.majiwa@cgnet.com  
Seq primer: T3 primer.

Location/Qualifiers  
1. 299  
/organism="Trypanosoma brucei rhodesiense"  
/db\_xref="taxon:31286"  
/clone\_lib="MVAT4 bloodstream form of serodeme WRATat1.1"  
/note="Vector: Lambda ZAP II (Stratagene); Site:1: EcoRI;  
Site:2: XhoI; The mRNA was purified from a cloned  
population of bloodstream trypanosomes reexpressing the  
MVAT4 metacyclic variant surface glycoprotein (VSG). A  
unidirectional oligo dt-primer EcoRI/XhoI cDNA library was  
constructed in lambda ZAP II (Stratagene)."  
97 a 60 c 94 g 48 t

BASE COUNT  
ORIGIN

Query Match 11.3%; Score 18; DB 9; Length 299;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 gctgaggttctgctgtg 128

|||||

Db 135 GCTGAGGTGCTGCTGTG 118

RESULT 16  
BF903506

LOCUS BF903506 303 bp mRNA linear EST 18-JAN-2001  
 DEFINITION IL2-WT0179-181200-287-F06 WT0179 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF903506  
 VERSION BF903506.1 GI:12295069  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 303)  
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-WT0179-181200-287-F06&t3=2000-12-18&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 12  
 High quality sequence stop: 283.

FEATURES  
 source  
 1..303  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="WT0179"  
 /dev\_stage="Adult"  
 /note="Organ: marrow; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 BASE COUNT 46 a 64 c 103 g 90 t  
 ORIGIN  
 Query Match 11.3%; Score 18; DB 10; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 80 ctggctgagggaacatgg 97  
 Db 214 CTGGCTGAGGGAACATGG 231  
 RESULT 17  
 BH127062  
 LOCUS G-10g13 r Maize Random Small-insert Genomic Library Zea mays  
 DEFINITION G-10g13 r Maize Random Small-insert Genomic Library Zea mays  
 ACCESSION BH127062  
 VERSION BH127062.1 GI:14994894  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 375)  
 AUTHORS Meyers, B.C., Tingey, S.V. and Morgante, M.  
 TITLE Abundance, distribution and transcriptional activity of repetitive elements in the maize genome  
 JOURNAL Genome Res. 11 (10), 1660-1676 (2001)  
 MEDLINE 21475670  
 COMMENT Contact: Morgante M  
 Suite 200  
 Dupont Genomics  
 PO Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302 631 2638  
 Fax: 302 631 2607  
 Email: Michele.morgante@usa.dupont.com  
 Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected.  
 Seq primer: M13reverse  
 Class: Shotgun.  
 Location/Qualifiers  
 1..375  
 /organism="Zea mays"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Random Small-insert Genomic Library"  
 /clone="G-10g13"  
 /sex="hermaphrodite"  
 /tissue\_type="leaf"  
 /cell\_type="Young leaf"  
 /dev\_stage="seedling"  
 /note="Vector: pCR-Script; Total genomic DNA was nebulized ; ends were polished with pfu polymerase and the fragments cloned into pCR-Script."  
 BASE COUNT 99 a 74 c 84 g 111 t 7 others  
 ORIGIN  
 Query Match 11.3%; Score 18; DB 12; Length 375;  
 Best Local Similarity 100.0%; Pred. No. 81;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 84 ctgaggggaacatggcatg 101  
 Db 7 CTGAGGGAACATGGCATG 24  
 RESULT 18  
 BF911983  
 LOCUS IL2-UT0073-121100-231-A10 UT0073 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION IL2-UT0073  
 ACCESSION BF911983  
 VERSION BF911983.1 GI:12303441  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 397)  
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=IL2&l2=IL2-UT0073-121100-231-A10&t3=2000-11-12&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 372.

#### FEATURES

Location/Qualifiers  
 1..397  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="UT0073"  
 /dev\_stage="Adult"  
 /note="Organ: uterus tumor; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 75 a 112 c 87 g 123 t

#### BASE COUNT

ORIGIN

Query Match 11.3%; Score 18; DB 10; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 gctgctgtggaagaacct 137  
 |||||  
 Db 57 GCTGCTGTGGAAGACCT 74

#### RESULT 19

BH396354/c  
 LOCUS BH396354 529 bp DNA linear GSS 11-DEC-2001  
 DEFINITION AG-ND-161J6.TF ND-TAM Anopheles gambiae genomic clone AG-ND-161J6,  
 DNA sequence.  
 ACCESSION BH396354  
 VERSION BH396354.1 GI:17342495  
 KEYWORDS GSS.  
 SOURCE African malaria mosquito.  
 ORGANISM Anopheles gambiae

#### REFERENCE

AUTHORS Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.  
 TITLE Direct Submission of BAC-end sequences from Anopheles gambiae  
 JOURNAL Unpublished (2001)  
 COMMENT Other GSSs: AG-ND-161J6.TR

Contact: Brendan J Loftus  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0208  
 Fax: 301 838 3543  
 Email: b.loftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by  
 F.H. Collins and sequenced by The Institute for Genomic Research  
 (TIGR). The BAC library was generated from A. gambiae PEST strain  
 DNA. All DNA was extracted from newly hatched first instar larvae  
 to minimize the inclusion of DNA from microorganisms that inhabit  
 the gut. The DNA is derived from mixed sexes of larvae. The BAC  
 library was constructed at Texas A&M University BAC Center  
 University, College Station, Texas 77843-2123, USA using a HindIII  
 partial digest.

Seq primer: M13 For

#### FEATURES

Class: BAC ends.  
 Location/Qualifiers  
 1..529

/organism="Anopheles gambiae"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="AG-ND-161J6"

/clone\_lib="ND-TAM"

/note="Vector: pECBAC1; Site\_1: HindIII"

BASE COUNT 122 a 121 c 151 g 135 t

#### ORIGIN

Query Match 11.3%; Score 18; DB 12; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 acttcagaagaagacaa 156  
 |||||

Db 206 ACTTTCAGAAGACAA 189

#### RESULT 20

AQ776697/c  
 LOCUS AQ776697 532 bp DNA linear GSS 29-JUL-1999  
 DEFINITION HS-2148\_B2\_H11\_T7C CIT Approved Human Genomic Sperm Library D Homo  
 sapiens genomic clone Plate-2148 Col=22 Row=P, DNA sequence.

ACCESSION AQ776697.1 GI:5656425

VERSION AQ776697

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 532)  
 AUTHORS Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 2148 row: P column: 22

Seq primer: T7

Class: BAC ends

High quality sequence stop: 532.

Location/Qualifiers

1..532

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="Plate-2148 Col=22 Row=P"

/clone\_lib="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in

E-Coli DH10B"

BASE COUNT 200 a 94 c 83 g 141 t 14 others

#### ORIGIN

Query Match 11.3%; Score 18; DB 12; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 gaggaacatggcatgtt 103  
 |||||

Db 226 GAGGGAACATGGCATGTT 209

JOURNAL  
COMMENT

Unpublished (1999)  
Other GSSs: RPCI-23-70H19.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jgong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
Plate: 70 row: H column: 19  
Seq primer: w7  
Class: BAC ends.

## Location/Qualifiers

1. .554  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-70H19"  
/clone\_lib="RPCI-23"  
/sex="Female"  
/lab\_host="DH10B"  
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT  
ORIGIN

141 a 129 c 131 g 153 t

## Query Match

Best Local Similarity 11.3%; Score 18; DB 12; Length 554;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 cagctgaggttctgctg 126  
|||||

Db 407 CAGCTGAGGTGCTGCTG 390

## RESULT 23

AZ510640/c

LOCUS

DEFINITION

1M0355G15F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0355G15 F, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

558 bp DNA linear GSS 05-OCT-2000  
AZ510640  
1M0355G15F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0355G15 F, DNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5506

## RESULT 21

AQ779444

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

AQ779444 532 bp DNA linear GSS 02-AUG-1999  
HS\_2001\_A2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=8 Row=K, DNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (1999)  
Other GSSs: RPCI-23-70H19.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jgong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
Plate: 70 row: H column: 19  
Seq primer: w7  
Class: BAC ends.

FEATURES  
source

1. .532  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=2001 Col=8 Row=K"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"  
High quality sequence stop: 532.  
Location/Qualifiers

BASE COUNT  
ORIGIN

155 a 86 c 156 g 126 t 9 others

## Query Match

Best Local Similarity 11.3%; Score 18; DB 12; Length 532;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ttgctgctgtggaagaac 135  
|||||

Db 372 TTGCTGCTGTGGAAGAAC 369

## RESULT 22

AZ236353/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

554 bp DNA linear GSS 14-JUN-2000  
AZ236353  
RPCI-23-70H19.TV RPCI-23 Mus musculus genomic clone RPCI-23-70H19, DNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5506

Tel: 801 585 7177  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0355 row: G column: 15  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 558.

# FEATURES

Location/Qualifiers  
 1..558

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0355M15"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 189 a 110 c 86 g 173 t  
 ORIGIN

Query Match 11.3%; Score 18; DB 12; Length 558;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ttgctgctgtggaagaac 135  
 ||||||||||||||||  
 Db 255 TTGCTGCTGTGGAAGAAC 238

# RESULT 24

AZ510673/c  
 LOCUS AZ510673 566 bp DNA linear GSS 05-OCT-2000  
 DEFINITION IM0355M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0355M15 F, DNA sequence.

ACCESSION AZ510673  
 VERSION AZ510673.1 GI:10691989  
 KEYWORDS GSS.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 566)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0355 row: M column: 15  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 566.

# FEATURES

Location/Qualifiers  
 1..566

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0355M15"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 193 a 103 c 85 g 185 t  
 ORIGIN

Query Match 11.3%; Score 18; DB 12; Length 566;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ttgctgctgtggaagaac 135  
 ||||||||||||||||  
 Db 233 TTGCTGCTGTGGAAGAAC 216

# RESULT 25

AZ720413/c  
 LOCUS AZ720413 599 bp mRNA linear EST 30-DEC-1997  
 DEFINITION ET2347 trypanosoma brucei rhodesiense ZAP II library Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence.

ACCESSION AA720413  
 VERSION AA720413.1 GI:2734023  
 KEYWORDS EST.

SOURCE Trypanosoma brucei rhodesiense.  
 ORGANISM Trypanosoma brucei rhodesiense

REFERENCE 1 (bases 1 to 599)  
 AUTHORS Ullu,E. and Tschudi,C.

TITLE Expressed sequence tags from procyclic Trypanosoma brucei rhodesiense cDNA clones

JOURNAL Unpublished (1997)  
 COMMENT Contact: Ullu E  
 Department of Internal Medicine, Section of Infectious Diseases  
 Yale University School of Medicine

P.O. Box 208022, 333 Cedar Street, New Haven, CT 06520-8022, USA  
 Fax: 203 785 3864  
 Email: elisabetta.ullu@yale.edu  
 Seq primer: SK.

```

FEATURES
  source
    Location/Qualifiers
      1..599
        /organism="Trypanosoma brucei rhodesiense"
        /strain="vfat 1.1"
        /db_xref="taxon:31286"
        /clone_lib="trypanosoma brucei rhodesiense ZAP II library"
        /dev_stage="insect form"
        /note="Vector: lambda ZAP II; Site_1: Eco RI; Site_2: Xho I; A unidirectional oligo dt-primered cDNA library was constructed in lambda ZAP II. Clones were selected using the criteria of low reactivity with a total cDNA probe."
BASE COUNT      167 a 136 c 131 g 127 t 38 others
ORIGIN

Query Match      11.3%; Score 18; DB 9; Length 599;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 gctgaggttgctgctgtg 128
|||||
Db 293 GCTGAGGTTGCTGCTGTG 276

RESULT 26
AL652524
LOCUS      AL652524 XGC-gastrula silurana tropicalis cDNA clone TGas028h10 5',
DEFINITION mRNA sequence.
ACCESSION AL652524
VERSION   AL652524.1 GI:17663079
KEYWORDS EST.
SOURCE    western clawed frog.
ORGANISM Silurana tropicalis
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
           Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 631)
AUTHORS   Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
TITLE     Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL   Unpublished (2001)
COMMENT   Contact: Huckle E
           Sanger Centre
           Hinxton, Cambridgeshire, CB10 1SA, UK
           Email: tropesanger.ac.uk
           Sanger Xenopus tropicalis EST project 2001
           TROPICALIS_SEQUENCE_ID: TGas028h10.sp6
           Sequencing primer: SP6
           This sequence is from a Xenopus Gene Collection (XGC) library
           constructed by Aaron M. Zorn.
FEATURES
  source
    Location/Qualifiers
      1..631
        /organism="Silurana tropicalis"
        /db_xref="taxon:8364"
        /clone="TGas028h10"
        /clone_lib="XGC-gastrula"
        /dev_stage="gastrula (stages 10.5-13 mixed)"
        /lab_host="Escherichia coli XL1-blue"
        /note="Vector: pCSI107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCSI107 with EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT      189 a 171 c 161 g 110 t
ORIGIN

Query Match      11.3%; Score 18; DB 9; Length 631;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 gagccacacgctggcgct 78
|||||
Db 61 gagccacacgctggcgct 78
|||||

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Db 78 GAGCCACACGCTGGCGT 95

RESULT 27
BB614720/c
LOCUS      BB614720 RIKEN full-length enriched, adult male testis Mus musculus
DEFINITION cDNA clone 4921533D20 5', mRNA sequence.
ACCESSION BB614720
VERSION   BB614720.1 GI:16455076
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 645)
AUTHORS   Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
           Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,
           M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
           Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
           D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
           Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
           Muramatsu, M. and Hayashizaki, Y.
TITLE     RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
JOURNAL   Unpublished (2001)
COMMENT   Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center (GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@gsc.riken.go.jp.
           URL: http://genome.gsc.riken.go.jp/
           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
           M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
           Normalization and subtraction of cap-trapper-selected cDNAs to
           prepare full-length cDNA libraries for rapid discovery of new
           genes. Genome Res. 10 (10), 1617-1630 (2000)
           wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
           Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura,
           S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
           Hayashizaki, Y.
           RIKEN integrated sequence analysis (RISA) system--384-format
           sequencing pipeline with 384 multicapillary sequencer. Genome Res.
           10 (11), 1757-1771 (2000)
           Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
           Y. and Hayashizaki, Y.
           Computer-based methods for the mouse full-length cDNA
           encyclopedia: real-time sequence clustering for construction of a
           nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
           Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alizawa,
           K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
           Hayashizaki, Y.
           Computational Analysis of Full-Length Mouse cDNAs Compared with
           Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
           Please visit our web site (http://genome.gsc.riken.go.jp) for
           further details.
           e mouse tissues.
           Location/Qualifiers
             1..645
               /organism="Mus musculus"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="4921533D20"
               /clone_lib="RIKEN full-length enriched, adult male testis"
               /sex="male"
               /tissue_type="testis"
               /dev_stage="adult"
               /lab_host="SOLR"
               /note="Site_1: XhoI; Site_2: BamHI; cDNA library was
               prepared and sequenced in Mouse Genome Encyclopedia
               Project of Genome Exploration Research Group in Riken

```



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DEFINITION   fm58c10.y1 zebrafish adult retina cDNA Danio rerio cDNA clone
              4199443 5' similar to SW:GBT1_BOVIN P04695 GUANINE
              NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 SUBUNIT ;, mRNA sequence.
ACCESSION    BG308188
VERSION      BG308188.1  GI:13105715
KEYWORDS     EST.
SOURCE       zebrafish.
ORGANISM     Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
              ; Cyprinidae; Danio.
REFERENCE    1 (bases 1 to 654)
AUTHORS      Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
              , S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
              , K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
              Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
              Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
              and Wilson, R.
TITLE        WashU Zebrafish EST Project 1998
JOURNAL      Unpublished (1998)
COMMENT      Other_ESTs: fm58c10.x1
              Contact: Stephen L. Johnson
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: zbrafish@wustl.edu
              Library constructed by: Chandra Tucker and Gregory Niemi DNA
              Sequencing by: Washington University Genome Sequencing Center Clone
              distribution: ResourceZentrumPrimatDatenbank, Berlin, Germany
              (web address: www.rzpd.de)
              Seq primer: T3 ET from Amersham
              High quality sequence stop: 410.
              Location/Qualifiers
              1..654
                /organism="Danio rerio"
                /strain="wild-type"
                /db_xref="taxon:7955"
                /clone="4199443"
                /clone_lib="Zebrafish adult retina cDNA"
                /sex="mixed"
                /dev_stage="1-2 years"
                /lab_host="E.Coli XL1-Blue MRF" (XL1-Blue MRF')
                /note="Vector: Lambda ZAP II (pBluescript SK-); Site_1:
              EcoRI; Site_2: SalI; This zebrafish library was
              constructed by Dr. Susan E. Brockerhoff (email:
              sbrocker@eu.washington.edu) RZPD library number: 760"
BASE COUNT   189 a 150 c 170 g 145 t
ORIGIN

```

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 672)  
 Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.  
 Direct Submission of BAC-end sequences from Anopheles gambiae  
 Unpublished (2001)  
 Contact: Brendan J Loftus  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0208  
 Fax: 301 838 3543  
 Email: bjloftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by  
 F.H. Collins and sequenced by The Institute for Genomic Research  
 (TIGR). The BAC library was generated from A. gambiae PEST strain  
 DNA. All DNA was extracted from newly hatched first instar larvae  
 to minimize the inclusion of DNA from microorganisms that inhabit  
 the gut. The DNA is derived from mixed sexes of larvae. The BAC  
 library was constructed at Texas A&M University BAC Center  
 University, College Station, Texas 77843-2123, USA using a HindIII  
 partial digest.

Seq primer: M13 For

Class: BAC ends.

Location/Qualifiers  
 1..672

/organism="Anopheles gambiae"  
 /strain="PEST"  
 /db\_xref="taxon:7165"  
 /clone="AG-ND-165M6"  
 /clone\_lib="ND-TAM"  
 /note="Vector: pECBAC1; Site\_1: HindIII"  
 176 a 155 c 160 g 181 t

## BASE COUNT ORIGIN

Query Match 11.3%; Score 18; DB 12; Length 672;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttaatgaccagccacggg 18  
 |||||  
 Db 612 TTATGACCCACGCGG 595

## RESULT 32 AW565995/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AW565995 683 bp mRNA linear EST 19-JUL-2000  
 LG1\_354\_G11\_g1\_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA  
 sequence.  
 AW565995 GI:7219873  
 EST.  
 SORGHUM  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 683)  
 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.  
 An EST database from Sorghum: light-grown seedlings  
 Unpublished (2000)  
 Contact: Cordonnier-Pratt MM  
 Department of Botany  
 The University of Georgia  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 542 1805  
 Email: mmpratt@uga.edu

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

Sequences have been trimmed to exclude PolyA, vector and regions  
 below Phred quality 16. The threshold for highest quality sequence  
 is 20.  
 Seq primer: T7  
 High quality sequence start: 4  
 High quality sequence stop: 667

## FEATURES source

Query Match 11.3%; Score 18; DB 10; Length 654;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 aagaacctcacttcaga 147  
 |||||  
 Db 635 AAGAACCTCACCCTTCAGA 652

## RESULT 31 BH375609/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BH375609 672 bp DNA linear GSS 10-DEC-2001  
 AG-ND-165M6.TF ND-TAM Anopheles gambiae genomic clone AG-ND-165M6,  
 DNA sequence.  
 BH375609  
 BH375609.1 GI:17321751  
 GSS.  
 African malaria mosquito.  
 Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae  
 ; Anopheles.

```

POLYA=No.
FEATURES
  source
    1..683
    /organism="Sorghum bicolor"
    /clone_lib="Light grown 1 (LG1)"
    /note="Organ: 10- to 14-day-old light-grown (greenhouse)
    seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
    : The library was made from poly-A RNA in the cloning
    vector lambda ZAP II. Clones to be sequenced were
    prepared by mass excision."
  BASE COUNT
  ORIGIN
    206 a 123 c 164 g 189 t 1 others
    11.38; Score 18; DB 9; Length 683;
    Query Match
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 aagaacctcacttcaga 147
|||||
Db 553 AAGAACCTCACTTTCAGA 536

RESULT 33
LOCUS AL648437 689 bp mRNA linear EST 13-DEC-2001
DEFINITION AL648437 XGC-gastrula Silurana tropicalis cDNA clone TCas033121 5',
mRNA sequence.
ACCESSION AL648437
VERSION AL648437.1 GI:17657152
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 689)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
Sanger Centre
Hinxtion, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TCas033121.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
  source
    1..689
    /organism="Silurana tropicalis"
    /db_xref="taxon:8364"
    /clone="TCas033121"
    /clone_lib="XGC-gastrula"
    /dev_stage="gastrula (stages 10.5-13 mixed)"
    /lab_host="Escherichia coli XL1-blue"
    /note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
    was oligo dt primed from 5ug of poly A+ RNA from stages
    10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
    into pCS107 with EcoRI at the 5' end and NotI at the 3'
    end."
  BASE COUNT
  ORIGIN
    184 a 193 c 185 g 127 t
    11.38; Score 18; DB 9; Length 689;
    Query Match
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 gagccacacgctggcgct 78
|||||

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Db 173 GAGCCACACGCTGGCGCT 190

RESULT 34
LOCUS AV868908 693 bp mRNA linear EST 08-NOV-2001
DEFINITION AV868908 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone rcieg35d09 3', mRNA sequence.
ACCESSION AV868908
VERSION AV868908.1 GI:16856432
KEYWORDS EST.
SOURCE Ciona intestinalis.
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 693)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@scidian.zool.kyoto-u.ac.jp.
FEATURES
  source
    1..693
    /organism="Ciona intestinalis"
    /db_xref="taxon:7719"
    /clone="rcieg35d09"
    /clone_lib="Nori Satoh unpublished cDNA library, egg"
    /tissue_type="whole animal"
    /dev_stage="egg"
  BASE COUNT
  ORIGIN
    195 a 142 c 120 g 235 t 1 others
    11.38; Score 18; DB 9; Length 693;
    Query Match
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 cctcactttcagaagaag 152
|||||
Db 247 CCTCACTTCAGAGAAG 264

RESULT 35
LOCUS BI254723 712 bp mRNA linear EST 17-JUL-2001
DEFINITION BI254723 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123378 5',
mRNA sequence.
ACCESSION BI254723
VERSION BI254723.1 GI:14807426
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11301 row: h column: 03

```

High quality sequence stop: 710.  
Location/Qualifiers  
1..712

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5123378"  
/clone\_lib="NIH\_MGC\_12"  
/tissue\_type="cervical carcinoma cell line"  
/lab\_host="DH10B"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.4 kb. Library prepared by Life  
Technologies."

BASE COUNT 197 a 176 c 176 g 163 t  
ORIGIN

Query Match 11.3%; Score 18; DB 10; Length 712;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 gctgctgaggaacatg 96  
|||||

Db 263 GCTGGCTGAGGAACATG 246

RESULT 36  
BI906710/c 796 bp mRNA linear EST 16-OCT-2001  
LOCUS BI906710.1 GI:16169467  
DEFINITION 603064430f1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5213695 5',  
mRNA sequence.

ACCESSION BI906710  
VERSION BI906710.1  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 796)

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

TITLE Contact: Robert Strausberg, Ph.D.

JOURNAL Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

COMMENT Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11536 row: k column: 08

High quality sequence stop: 787.

Location/Qualifiers

FEATURES

source

1..796  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5213695"  
/clone\_lib="NIH\_MGC\_118"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."

BASE COUNT 209 a 206 c 192 g 189 t

ORIGIN

Query Match 11.3%; Score 18; DB 10; Length 796;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 agaacctcacttcagaa 148  
|||||

Db 20 AGAACCTCACTTCAGAA 3

RESULT 37

BI181298

LOCUS

DEFINITION 018\_I\_20-rev SmbAC1 Schistosoma mansoni genomic clone 018I20 5',  
DNA sequence.

ACCESSION BI181298

VERSION BI181298.1 GI:16284183

KEYWORDS GSS.

SOURCE Schistosoma mansoni.

ORGANISM Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 809)

AUTHORS Le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams,  
D.L., Johnston, D., LovVerde, P.T. and Le Paslier, D.

TITLE Construction and characterization of a Schistosoma mansoni  
bacterial artificial chromosome library

JOURNAL Genomics 65 (2), 87-94 (2000)

MEDLINE 20247247

COMMENT Other\_GSSs: 018\_I\_20-21

Contact: Pierce RJ

INSERM U 167

Institut Pasteur de Lille

1 rue du Professeur A. Calmette, 59019-Lille, France

Tel: (33) (0)3 20877783

Fax: (33) (0)3 20877888

Email: [Raymond.Pierce@pasteur-lille.fr](mailto:Raymond.Pierce@pasteur-lille.fr)

CNS sequencing ID=DGAA018BE10BP1 Bases 167-538 have 84% identity

to S.mansoni EST AW061395.1 from base 25-393.

Plate: 018 row: I column: 20

Seq primer: M13 reverse primer

Class: BAC ends

High quality sequence stop: 809.

FEATURES

source

1..809

/organism="Schistosoma mansoni"

/strain="Puerto-Rican"

/db\_xref="taxon:6183"

/clone="018I20"

/clone\_lib="SmbAC1"

/sex="mixed"

/dev\_stage="cercariae"

/lab\_host="Biomphalaria glabrata"

/note="Vector: pBelOBAC 11; Site\_1: Hind III; Partially  
Hind III digested and size-selected S. mansoni cercarial  
DNA was ligated into Hind III digested pBelOBAC 11 vector  
and used to transform E. coli DH10B. The complete library  
contains 23808 clones from 4 independent  
sizing-ligation-transformations. Average insert size  
ranges from 70-127 kb and genome coverage is 7.9-fold."

BASE COUNT 313 a 155 c 109 g 229 t

ORIGIN

Query Match 11.3%; Score 18; DB 12; Length 809;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 ttcaagaagaacaaaca 159  
|||||

Db 536 TTCAGAGAAGACAAACA 553